

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 18:29:37 ; Search time 9967.36 Seconds

(Without alignments)
42.201 Million cell updates/sec

Title: US-09-631-709-5

Perfect score: 1 caagaattctcatgttgacagct 24

Sequence: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 17159718 seqs, 876320856 residues

Total number of hits satisfying chosen parameters: 34319436

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	100.0	24	24 US-09-631-709-5	Sequence 5, Appl 1
2	24	100.0	29	1 PCT-US00-2712-1	Sequence 11, Appl 1
3	24	100.0	57	15 US-09-132-331-13	Sequence 7, Appl 1
4	24	100.0	4752	6 US-08-299-0922A-7	Sequence 7, Appl 1
5	24	100.0	4752	12 US-08-819-723-7	Sequence 7, Appl 1
6	24	100.0	4754	6 US-08-299-0922A-5	Sequence 5, Appl 1
7	24	100.0	4754	12 US-08-819-723-5	Sequence 5, Appl 1
8	24	100.0	5005	7 US-08-398-139B-60	Sequence 60, Appl 1
9	24	100.0	6364	19 US-09-517-466-151	Sequence 151, App
10	24	100.0	6364	19 US-09-517-466-145	Sequence 145, App
11	24	100.0	6422	19 US-09-517-466-142	Sequence 142, App
12	24	100.0	6652	19 US-09-517-466-153	Sequence 153, App
13	24	100.0	6675	19 US-09-517-466-144	Sequence 144, App
14	24	100.0	6675	19 US-09-517-466-152	Sequence 152, App
15	24	100.0	7013	19 US-09-517-466-143	Sequence 143, App
16	24	100.0	7114	19 US-09-517-466-181	Sequence 181, App
17	24	100.0	8540	8 US-08-431-644A-12	Sequence 12, Appl 1
18	24	100.0	8540	8 US-08-487-283A-4	Sequence 4, Appl 1
19	24	100.0	8545	8 US-08-487-283A-4	Sequence 4, Appl 1
20	24	100.0	8575	9 US-08-541-572-6	Sequence 6, Appl 1
21	24	100.0	8932	6 US-08-252-493A-8	Sequence 8, Appl 1
22	24	100.0	10332	18 US-09-423-838-13	Sequence 13, Appl 1
23	24	100.0	10380	15 US-09-040-961-1	Sequence 1, Appl 1
24	24	100.0	10380	15 US-09-130-115-1	Sequence 1, Appl 1
25	24	100.0	11265	18 US-09-402-020-1	Sequence 1, Appl 1
26	24	100.0	16080	18 US-09-471-669-48	Sequence 48, Appl 1
27	24	100.0	16080	19 US-09-501-708-48	Sequence 48, Appl 1
28	24	100.0	16080	29 US-09-723-739-48	Sequence 48, Appl 1
29	24	100.0	16080	29 US-09-724-566-48	Sequence 48, Appl 1
30	24	100.0	16080	29 US-09-724-568-48	Sequence 48, Appl 1
31	24	100.0	16080	29 US-09-724-569-48	Sequence 48, Appl 1
32	24	100.0	16080	29 US-09-724-571-48	Sequence 48, Appl 1
33	24	100.0	19798	29 US-09-721-479B-10	Sequence 10, Appl 1
34	24	100.0	19912	29 US-09-721-479B-8	Sequence 8, Appl 1
35	24	100.0	20160	29 US-09-721-479B-12	Sequence 12, Appl 1
36	24	100.0	20217	29 US-09-721-479B-16	Sequence 16, Appl 1
37	24	100.0	20247	29 US-09-721-479B-18	Sequence 18, Appl 1
38	24	100.0	20316	29 US-09-721-479B-14	Sequence 14, Appl 1
39	24	100.0	34303	1 PCT-US97-19541-4	Sequence 4, Appl 1
40	24	100.0	34303	13 US-08-940-443-4	Sequence 4, Appl 1
41	24	95.8	5076	1 PCT-US01-21701-8	Sequence 8, Appl 1

42 23 95.8 5076 32 US-09-902-537-8 Sequence 8, Appl
43 23 95.8 6989 1 PCT-US01-21701-11 Sequence 11, Appl
44 23 95.8 6989 32 US-09-902-537-11 Sequence 11, Appl
45 23 95.8 12379 32 US-09-902-537-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-631-709-5
; Sequence 5, Application US/09631709
; GENERAL INFORMATION:
; APPLICANT: KYOMA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: PROCESS FOR PRODUCING GDP-FUCOSE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/631,709
; CURRENT FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver.2.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-631-709-5

Query Match 100.0%; Score 24; DB 24; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcattgttgacagct 24
DB 1 caagaatcctcattgttgacagct 24

RESULT 2
PCT-US00-27212-1
; Sequence 1, Application PC/TUS0027212
; GENERAL INFORMATION:
; APPLICANT: MOJIMAR-KIMBER, KATHERINE
; APPLICANT: TOYOZUMI, TAKANE
; TITLE OF INVENTION: REPLICATION SELECTIVE ADENOVIRUSES FOR USE IN CANCER
; TITLE OF INVENTION: THERAPY
; FILE REFERENCE: 22253-66146
; CURRENT APPLICATION NUMBER: PCT/US00/27212
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/157,224
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR generated
; OTHER INFORMATION: oligonucleotides
PCT-US00-27212-1

Query Match 100.0%; Score 24; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcattgttgacagct 24
DB 4 caagaatcctcattgttgacagct 27

RESULT 3

US-09-132-231-13
; Sequence 13, Application US/09132231A
; GENERAL INFORMATION:
; APPLICANT: HORWITZ, Marshall S.
; APPLICANT: LOEB, Lawrence A.
; TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL DNA SEQUENCES WITH
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY
; FILE REFERENCE: 032425-001
; CURRENT APPLICATION NUMBER: US/09/132,231A
; CURRENT FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: US 08/316,415
; PRIOR FILING DATE: 1994-09-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-132-231-13

Query Match 100.0%; Score 24; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatcctcattgttgacagct 24
DB 1 caagaatcctcattgttgacagct 24

RESULT 4
US-08-299-092A-7
; Sequence 7, Application US/08299092A
; GENERAL INFORMATION:
; APPLICANT: Coughlin, Richard T.
; APPLICANT: Ma, Jinneng
; TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria
; TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter
; TITLE OF INVENTION: Assay for Borrelia Activity of Antisera
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,092A
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/025,379
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleisher, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 0614.1080002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 1..939
US-08-299-092A-7

Query Match 100.0%; Score 24; DB 6; Length 4752;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatctcatgtttgacagct 24
|||||
Db 4045 CAAGAATCTCATGTTCACAGCT 4068

RESULT 5
US-08-819-723-7
Sequence 7, Application US/08819723
GENERAL INFORMATION:
APPLICANT: Coughlin, Richard T.
APPLICANT: Ma, Jiansheng
APPLICANT: Marciani, Dante J.
TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria
TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter
TITLE OF INVENTION: Assay for Borrelia Activity of Antisera
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,723
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,092
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Flesher, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 1673.1080003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4752 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..939
US-08-819-723-7

Query Match 100.0%; Score 24; DB 12; Length 4752;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatctcatgtttgacagct 24
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Db 4045 CAAGAATCTCATGTTCACAGCT 4068

RESULT 6
US-08-299-092A-5
Sequence 5, Application US/08299092A
GENERAL INFORMATION:
APPLICANT: Coughlin, Richard T.
APPLICANT: Ma, Jiansheng
APPLICANT: Marciani, Dante J.
TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria
TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter
TITLE OF INVENTION: Assay for Borrelia Activity of Antisera
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,092A
FILING DATE: 02-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/025,379
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Flesher, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0614.1080002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4754 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..870
US-08-299-092A-5

Query Match 100.0%; Score 24; DB 6; Length 4754;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatctcatgtttgacagct 24
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Db 4047 CAAGAATCTCATGTTCACAGCT 4070

RESULT 7
US-08-819-723-5
Sequence 5, Application US/08819723
GENERAL INFORMATION:
APPLICANT: Coughlin, Richard T.
APPLICANT: Ma, Jiansheng
APPLICANT: Marciani, Dante J.
TITLE OF INVENTION: Methods of Inducing Immunity to Bacteria
TITLE OF INVENTION: Causing Lyme Disease and a Simple Colorimetric Microtiter
TITLE OF INVENTION: Assay for Borrelia Activity of Antisera
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington

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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,723
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,092
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pleshner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 1673.1080003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4754 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..870
US-08-819-723-5

Query Match
Best local similarity 100.0%; Score 24; DB 12; Length 4754;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatctcatgtttgacagct 24
Db 4047 CAAGAATCTCATGTTGACAGCT 4070

RESULT 8
US-08-398-139B-60/C
GENERAL INFORMATION:
SEQUENCE 60, Application US/08398139B
APPLICANT: Anderson, Carl W.
TITLE OF INVENTION: DNA-PK Assay
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: Brookhaven National Laboratory
STREET: Building 902C, P.O. Box 5000
CITY: Upton
STATE: New York
COUNTRY: USA
ZIP: 11973-5000
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM XT compatible
OPERATING SYSTEM: MS DOS Ver. 6.0
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,139B
FILING DATE: 3-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132,284
FILING DATE: 6-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324

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REFERENCE/DOCKET NUMBER: AUI 94-27
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 5005 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-398-139B-60

Query Match
Best local similarity 100.0%; Score 24; DB 7; Length 5005;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaatctcatgtttgacagct 24
Db 385 CAAGAATCTCATGTTGACAGCT 362

RESULT 9
US-09-517-466-151/C
GENERAL INFORMATION:
SEQUENCE 151, Application US/09517466
APPLICANT: Hartley, James
APPLICANT: Brasch, Michael
APPLICANT: Temple, Gary
APPLICANT: Cheo, David
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning
FILE REFERENCE: 0942.4680003
CURRENT APPLICATION NUMBER: US/09/517,466
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/122,389
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: US 60/126,049
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/136,744
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 151
LENGTH: 6264
TYPE: DNA
ORGANISM: PDEST23
FEATURE:
NAME/KEY: gene
LOCATION: (161)..(285)
OTHER INFORMATION: attR1
NAME/KEY: gene
LOCATION: (394)..(1053)
OTHER INFORMATION: cmr
NAME/KEY: gene
LOCATION: (1173)..(1257)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1395)..(1700)
OTHER INFORMATION: ccdb
NAME/KEY: gene
LOCATION: (1741)..(1865)
OTHER INFORMATION: attR2
NAME/KEY: gene
LOCATION: (1883)..(1911)
OTHER INFORMATION: his6
NAME/KEY: gene
LOCATION: (2574)..(3434)
OTHER INFORMATION: ampr
NAME/KEY: gene
LOCATION: (3583)..(4222)
OTHER INFORMATION: ori
US-09-517-466-151

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Query Match          100.0%; Score 24; DB 19; Length 6264;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgcacct 24
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DB 2371 CAAGAATTCTCATGTTTGACAGCT 2348

RESULT 10
US-09-517-466-145/c
; Sequence 145, Application US/09517466
; GENERAL INFORMATION:
; APPLICANT: Hartley, James
; APPLICANT: Brasch, Michael
; APPLICANT: Temple, Gary
; APPLICANT: Cheo, David
; TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning of
; FILE REFERENCE: 0942.4680003
; CURRENT APPLICATION NUMBER: US/09/517,466
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/122,389
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/126,049
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/136,744
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 145
; LENGTH: 6354
; TYPE: DNA
; ORGANISM: pDEST17
; FEATURE:
; NAME/KEY: gene
; LOCATION: (134)..(258)
; OTHER INFORMATION: attR1
; NAME/KEY: gene
; LOCATION: (367)..(1026)
; OTHER INFORMATION: Cmr
; NAME/KEY: gene
; LOCATION: (1146)..(1230)
; OTHER INFORMATION: Inactivated ccda
; NAME/KEY: gene
; LOCATION: (1368)..(1673)
; OTHER INFORMATION: ccdb
; NAME/KEY: gene
; LOCATION: (1714)..(1838)
; OTHER INFORMATION: attR2
; NAME/KEY: gene
; LOCATION: (2564)..(3421)
; OTHER INFORMATION: ampr
; US-09-517-466-145

Query Match          100.0%; Score 24; DB 19; Length 6354;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgcacct 24
    |||
DB 2361 CAAGAATTCTCATGTTTGACAGCT 2338

RESULT 11
US-09-517-466-142/c
; Sequence 142, Application US/09517466
; GENERAL INFORMATION:
; APPLICANT: Hartley, James
; APPLICANT: Brasch, Michael
; APPLICANT: Temple, Gary
; APPLICANT: Cheo, David

; TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning
; FILE REFERENCE: 0942.4680003
; CURRENT APPLICATION NUMBER: US/09/517,466
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/122,389
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/126,049
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/136,744
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142
; LENGTH: 6422
; TYPE: DNA
; ORGANISM: pDEST14
; FEATURE:
; NAME/KEY: gene
; LOCATION: (61)..(185)
; OTHER INFORMATION: attR1
; NAME/KEY: gene
; LOCATION: (435)..(1094)
; OTHER INFORMATION: Cmr
; NAME/KEY: gene
; LOCATION: (1214)..(1298)
; OTHER INFORMATION: Inactivated ccda
; NAME/KEY: gene
; LOCATION: (1436)..(1741)
; OTHER INFORMATION: ccdb
; NAME/KEY: gene
; LOCATION: (1782)..(1906)
; OTHER INFORMATION: attR2
; NAME/KEY: gene
; LOCATION: (2632)..(3489)
; OTHER INFORMATION: ampr
; US-09-517-466-142

Query Match          100.0%; Score 24; DB 19; Length 6422;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgcacct 24
    |||
DB 2429 CAAGAATTCTCATGTTTGACAGCT 2406

RESULT 12
US-09-517-466-153/c
; Sequence 153, Application US/09517466
; GENERAL INFORMATION:
; APPLICANT: Hartley, James
; APPLICANT: Brasch, Michael
; APPLICANT: Temple, Gary
; APPLICANT: Cheo, David
; TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning
; FILE REFERENCE: 0942.4680003
; CURRENT APPLICATION NUMBER: US/09/517,466
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/122,389
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/126,049
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/136,744
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 153
; LENGTH: 6652
; TYPE: DNA
; ORGANISM: pDEST25
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us-09-631-709-5.inpm

Page 6

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FEATURE:
NAME/KEY: gene
LOCATION: (720)..(844)
OTHER INFORMATION: atlr1
NAME/KEY: gene
LOCATION: (953)..(1612)
OTHER INFORMATION: cmr
NAME/KEY: gene
LOCATION: (1732)..(1816)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1954)..(2259)
OTHER INFORMATION: ccdb
NAME/KEY: gene
LOCATION: (2300)..(2424)
OTHER INFORMATION: atlr2
NAME/KEY: gene
LOCATION: (2432)..(2794)
OTHER INFORMATION: trx
US-09-517-466-153
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Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 6652;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
Db 3318 CAAGAATTCATGTTGACAGCT 3295
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RESULT 13
US-09-517-466-144/c
Sequence 144, Application US/09517466
GENERAL INFORMATION:
APPLICANT: Hartley, James
APPLICANT: Brasch, Michael
APPLICANT: Temple, Gary
APPLICANT: Cheo, David
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning of
FILE REFERENCE: 0942.4680003
CURRENT APPLICATION NUMBER: US/09/517,466
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/122,389
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: US 60/126,049
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/136,744
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 144
LENGTH: 6675
TYPE: DNA
ORGANISM: pDEST16
FEATURE:
NAME/KEY: gene
LOCATION: (104)..(457)
OTHER INFORMATION: trxa
NAME/KEY: gene
LOCATION: (461)..(585)
OTHER INFORMATION: atlr1
NAME/KEY: gene
LOCATION: (594)..(1353)
OTHER INFORMATION: cmr
NAME/KEY: gene
LOCATION: (1473)..(1557)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1695)..(2000)
OTHER INFORMATION: ccdb
NAME/KEY: gene
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LOCATION: (2041)..(2165)
OTHER INFORMATION: atlr2
US-09-517-466-144
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Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 6675;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
Db 2688 CAAGAATTCATGTTGACAGCT 2665
```

```
RESULT 14
US-09-517-466-152/c
Sequence 152, Application US/09517466
GENERAL INFORMATION:
APPLICANT: Hartley, James
APPLICANT: Brasch, Michael
APPLICANT: Temple, Gary
APPLICANT: Cheo, David
TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning
FILE REFERENCE: 0942.4680003
CURRENT APPLICATION NUMBER: US/09/517,466
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/122,389
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: US 60/126,049
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/136,744
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 152
LENGTH: 6961
TYPE: DNA
ORGANISM: pDEST24
FEATURE:
NAME/KEY: gene
LOCATION: (71)..(195)
OTHER INFORMATION: atlr1
NAME/KEY: gene
LOCATION: (304)..(963)
OTHER INFORMATION: cmr
NAME/KEY: gene
LOCATION: (1083)..(1167)
OTHER INFORMATION: inactivated ccda
NAME/KEY: gene
LOCATION: (1305)..(1610)
OTHER INFORMATION: ccdb
NAME/KEY: gene
LOCATION: (1651)..(1775)
OTHER INFORMATION: atlr2
NAME/KEY: gene
LOCATION: (1783)..(2451)
OTHER INFORMATION: GST
NAME/KEY: gene
LOCATION: (3181)..(4041)
OTHER INFORMATION: ampr
NAME/KEY: gene
LOCATION: (4190)..(4829)
OTHER INFORMATION: ori
US-09-517-466-152
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Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 6961;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgcagct 24
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Db 2978 CAAGAATTCATGTTGACAGCT 2955

RESULT 15

US-09-517-466-143/C
Sequence 143, Application US/09517466

GENERAL INFORMATION:

APPLICANT: Hartley, James
APPLICANT: Brasch, Michael
APPLICANT: Temple, Gary
APPLICANT: Cheo, David

TITLE OF INVENTION: Compositions and Methods for Use in Recombinational Cloning of

FILE REFERENCE: 0942.4680003

CURRENT APPLICATION NUMBER: US/09/517,466

PRIOR APPLICATION NUMBER: US 60/122,389

PRIOR FILING DATE: 1999-03-02

PRIOR APPLICATION NUMBER: US 60/126,049

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: US 60/136,744

PRIOR FILING DATE: 1999-05-28

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PatentIn version 3.0

SEQ ID NO 143

LENGTH: 7013

TYPE: DNA

ORGANISM: pDEST15

FEATURE:

NAME/KEY: gene

LOCATION: (108)..(776)

OTHER INFORMATION: GST

NAME/KEY: gene

LOCATION: (792)..(916)

OTHER INFORMATION: atcR1

NAME/KEY: gene

LOCATION: (1025)..(1537)

OTHER INFORMATION: Cmr

NAME/KEY: gene

LOCATION: (1804)..(1888)

OTHER INFORMATION: Inactivated ccdA

NAME/KEY: gene

LOCATION: (2026)..(2331)

OTHER INFORMATION: ccdB

NAME/KEY: gene

LOCATION: (2372)..(2496)

OTHER INFORMATION: atcR2

NAME/KEY: gene

LOCATION: (3233)..(4093)

OTHER INFORMATION: ampr

US-09-517-466-143

Query Match

Best Local Similarity 100.0%; Score 24; DB 19; Length 7013;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgacagct 24

Db 3030 CAAGAATTCATGTTGACAGCT 3007

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Job time: 18173 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 13:32:30 : Search time 176.03 Seconds
(without alignments)
30.878 Million cell updates/sec

Title: US-09-631-709-5
Perfect score: 24
Sequence: 1 caagattctcatgtttgacagct 24

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA :
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2: /cgn2_6/prodata/2/ina/5B.COMB.seq:*
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5: /cgn2_6/prodata/2/ina/PCBUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	35	1	US-07-985-690A-9	Sequence 9, Appl1
2	24	100.0	55	1	US-08-441-116-1	Sequence 1, Appl1
3	24	100.0	3918	2	US-08-495-500-2	Sequence 2, Appl1
4	24	100.0	5552	2	US-08-155-888-1	Sequence 1, Appl1
5	24	100.0	6623	2	US-08-244-434-36	Sequence 36, Appl1
6	24	100.0	6630	2	US-08-244-434-37	Sequence 37, Appl1
7	24	100.0	6727	2	US-08-125-462-2	Sequence 2, Appl1
8	24	100.0	6727	2	US-08-891-848-2	Sequence 2, Appl1
9	24	100.0	6799	2	US-08-125-462-5	Sequence 5, Appl1
10	24	100.0	6799	2	US-08-891-848-5	Sequence 5, Appl1
11	24	100.0	8540	5	PCT-US96-05611A-12	Sequence 12, Appl1
12	24	100.0	8575	5	PCT-US97-08258-6	Sequence 6, Appl1
13	24	100.0	8932	2	US-08-252-493C-8	Sequence 8, Appl1
14	24	100.0	8932	3	US-09-276-197-8	Sequence 8, Appl1
15	24	100.0	11616	1	US-08-196-259-2	Sequence 2, Appl1
16	24	100.0	34303	2	US-08-735-609-4	Sequence 4, Appl1
17	24	100.0	34303	2	US-08-735-609-4	Sequence 4, Appl1
18	24	100.0	34303	3	US-09-315-372-4	Sequence 4, Appl1
19	24	100.0	34303	3	US-09-244-752-4	Sequence 4, Appl1
20	24	100.0	34303	3	US-09-245-497-4	Sequence 4, Appl1
21	23	95.8	8501	4	US-08-793-900-1	Sequence 1, Appl1
22	22.4	93.3	6166	4	US-08-591-632-51	Sequence 51, Appl1
23	22.4	93.3	8157	1	US-08-358-160-65	Sequence 65, Appl1
24	22.4	93.3	8584	1	US-08-358-160-66	Sequence 66, Appl1
25	22.4	93.3	8590	1	US-08-358-160-70	Sequence 70, Appl1
26	22	91.7	7641	1	US-07-924-028A-5	Sequence 5, Appl1
27	21.4	89.2	1738	1	US-07-971-160-9	Sequence 9, Appl1

28	21.4	89.2	1738	1	US-08-336-241-9	Sequence 9, Appl1
29	21.4	89.2	1738	2	US-08-465-273-9	Sequence 9, Appl1
30	21.4	89.2	1738	2	US-09-119-024-9	Sequence 9, Appl1
31	21.4	89.2	1738	2	US-08-417-226-9	Sequence 9, Appl1
32	21.4	89.2	1738	4	US-09-196-131-9	Sequence 15, Appl1
33	21.4	89.2	10596	1	US-07-884-811-15	Sequence 15, Appl1
34	21.4	89.2	10596	1	US-07-885-971-15	Sequence 15, Appl1
35	21.4	89.2	10596	1	US-08-087-783A-15	Sequence 15, Appl1
36	21.4	89.2	10596	2	US-08-194-088B-15	Sequence 15, Appl1
37	21.4	89.2	10596	2	US-08-194-087-15	Sequence 15, Appl1
38	21.4	89.2	10596	5	PCT-US93-04648-15	Sequence 15, Appl1
39	21	87.5	31	4	US-08-416-544B-14	Sequence 14, Appl1
40	21	87.5	1130	2	US-08-613-965-1	Sequence 1, Appl1
41	21	87.5	1130	2	US-08-918-966-1	Sequence 1, Appl1
42	21	87.5	1130	3	US-08-921-655-1	Sequence 1, Appl1
43	21	87.5	5249	1	US-08-688-649-3	Sequence 3, Appl1
44	21	87.5	5249	1	US-08-688-649-4	Sequence 4, Appl1
45	21	87.5	7859	1	US-07-854-596B-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-07-985-690A-9
: Sequence 9, Application US/07985690A
: Patent No. 5376545
: GENERAL INFORMATION:
: APPLICANT: Yagasaki, Makoto
: APPLICANT: Ishino, Shuichi
: APPLICANT: Iwata, Kazuhisa
: APPLICANT: Azuma, Masaki
: APPLICANT: Teshiba, Sadao
: APPLICANT: Hasegawa, Masaru
: APPLICANT: Yamaguchi, Kazuo
: APPLICANT: Yano, Keiichi
: APPLICANT: Yokoo, Yoshiharu
: APPLICANT: Hashimoto, Yukio
: TITLE OF INVENTION: DNA CODING FOR URICASE AND PROCESS FOR
: TITLE OF INVENTION: PRODUCING URICASE
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
: STREET: Suite 600, 1919 Pennsylvania Avenue, N.W.
: City: Washington,
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20006
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
: COMPUTER: NEC PC-9801 Series
: OPERATING SYSTEM: MS-DOS Ver3.30 or Later
: SOFTWARE: PATENT AID
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/985,690A
: FILING DATE: 19921203
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP91/320525
: FILING DATE: 04-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Terry, David T.
: REGISTRATION NUMBER: 20178
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-828-0300
: TELEFAX: 202-828-0380
: TELEX: 440280
: INFORMATION FOR SEQ ID NO: 9 :
: SEQUENCE CHARACTERISTICS:
: LENGTH: 35 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear

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Page 2

MOLECULE TYPE: Other nucleic acid
SYNTHETIC DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-985-690A-9

Query Match 100.0%; Score 24; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattctcatgtttgacagct 24
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DB 4 CAAGAATTCATCTGTTGACAGCT 27

RESULT 2

US-08-441-116-1
Sequence 1, Application US/08441116
Patent No. 5641764
GENERAL INFORMATION:
APPLICANT: Martin, Roger F.
TITLE OF INVENTION: HALOGENATED DNA LIGAND
TITLE OF INVENTION: RADIOSENSITISERS FOR CANCER THERAPY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
COUNTRY: United States of America
ZIP: 22037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441.116
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,588
FILING DATE: 30-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kit, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: Q27431
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 393-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-441-116-1

Query Match 100.0%; Score 24; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattctcatgtttgacagct 24
|||||
DB 17 CAAGAATTCATCTGTTGACAGCT 40

US-08-495-500-2
Sequence 2, Application US/08495500
Patent No. 5962222
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Protein fusions for the translocation of
TITLE OF INVENTION: Apo-protein into the periplasmic space
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,500
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9301553.5
FILING DATE: 27-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO GB94/00161
FILING DATE: 27-JAN-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: circular
US-08-495-500-2

Query Match 100.0%; Score 24; DB 2; Length 3918;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattctcatgtttgacagct 24
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DB 2689 CAAGAATTCATCTGTTGACAGCT 2712

RESULT 4

US-08-155-888-1/c
Sequence 1, Application US/08155888
Patent No. 6066623
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE
TITLE OF INVENTION: AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Naval Medical Res. & Dev. Cnd.
STREET: Bldg. 1, T-12 8901 Wisconsin Ave.
CITY: Bethesda
STATE: Maryland
COUNTRY: USA
ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, A. David

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: REGISTRATION NUMBER: 24,743
: REFERENCE/DOCKET NUMBER: N.C. 75,851
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 295-6759
: TELEFAX: (202) 295-1022
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5552 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: circular
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: promoter
: LOCATION: 1..755
: IDENTIFICATION METHOD: experimental
: OTHER INFORMATION: /function="promoter"
: OTHER INFORMATION: /evidence=EXPERIMENTAL
: OTHER INFORMATION: /label=CMV-IE
: OTHER INFORMATION: /note="this feature acts as a promoter for any
: OTHER INFORMATION: downstream DNA sequence."
: OTHER INFORMATION: /citation=(12)]
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 933..2367
: IDENTIFICATION METHOD: experimental
: OTHER INFORMATION: /codon_start=933
: OTHER INFORMATION: /function="protein protective against malaria"
: OTHER INFORMATION: /product="protein"
: OTHER INFORMATION: /evidence=EXPERIMENTAL
: OTHER INFORMATION: /number=1
: OTHER INFORMATION: /label=IL2-CSP
: OTHER INFORMATION: /citation=(11)]
: PUBLICATION INFORMATION:
: AUTHORS: Sedegah, Martha
: AUTHORS: Hedstrom, Richard C.
: AUTHORS: Hoffman, Stephen L.
: TITLE: Vaccination with Plasmodium yoelii CS protein
: TITLE: plasmid DNA protects against malaria
: JOURNAL: Science
: PUBLICATION INFORMATION:
: AUTHORS: Cullen, Bryan R.
: TITLE: TRANS-ACTIVATION OF HUMAN IMMUNODEFICIENCY
: TITLE: VIRUS OCCURS VIA A BIMODAL MECHANISM
: JOURNAL: CELL
: VOLUME: 46
: PAGES: 973-982
: DATE: 26 SEP-1986
: RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4732
:
: US-08-155-888-1
:
: Query Match 100.0%; Score 24; DB 3; Length 5552;
: Best Local Similarity 100.0%; Pred. No. 0.019;
: Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 caagaattcctggttgacagct 24
: |||||||||||||||||||
: Db 3259 CAGAATTCTCATGTTGACAGCT 3236
:
: RESULT 5
: US-08-244-434-36
: Sequence 36, Application US/08244434
: Patent No. 5854004
: GENERAL INFORMATION:
: APPLICANT: Czeruliofsky, A.P.
: APPLICANT: Himmler, A.
: APPLICANT: Stratowa, C.
: APPLICANT: Weyer, U.
: APPLICANT: Lamche, H.
: APPLICANT: Sch fer, R.

```

```

: TITLE OF INVENTION: Process for Screening Substances Capable of
: TITLE OF INVENTION: Modulating a Receptor-Dependent Cellular Signal
: TITLE OF INVENTION: Transmission Path
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/244,434
: FILING DATE: 25-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/92/02718
: FILING DATE: PCT Filing Date: 25-NOV-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Esmond, Robert W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 0652.1340000/RWE
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6623 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: circular
: MOLECULE TYPE:
:
: US-08-244-434-36
:
: Query Match 100.0%; Score 24; DB 2; Length 6623;
: Best Local Similarity 100.0%; Pred. No. 0.02;
: Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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: QY 1 caagaattcctggttgacagct 24
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: Db 6529 CAGAATTCTCATGTTGACAGCT 6552
:
: RESULT 6
: US-08-244-434-37
: Sequence 37, Application US/08244434
: Patent No. 5854004
: GENERAL INFORMATION:
: APPLICANT: Czeruliofsky, A.P.
: APPLICANT: Himmler, A.
: APPLICANT: Stratowa, C.
: APPLICANT: Weyer, U.
: APPLICANT: Lamche, H.
: APPLICANT: Sch fer, R.
: TITLE OF INVENTION: Process for Screening Substances Capable of
: TITLE OF INVENTION: Modulating a Receptor-Dependent Cellular Signal
: TITLE OF INVENTION: Transmission Path
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,434
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/92/02718
FILING DATE: PCT Filing Date: 25-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1340000/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 6630 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-244-434-37

Query Match 100.0%; Score 24; DB 2; Length 6630;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgacgct 24
DB 6536 CAGCAATTCATGTTGACAGCT 6559

RESULT 7
US-08-125-462-2/c
Sequence 2, Application US/08125462
Patent No. 5840840
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,462
FILING DATE: 22-SEP-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-110-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..6727
OTHER INFORMATION: /standard_name="pET-11d-ANG-E6"
US-08-125-462-2

Query Match 100.0%; Score 24; DB 2; Length 6727;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgacgct 24
DB 1530 CAGCAATTCATGTTGACAGCT 1507

RESULT 8
US-08-891-848-2/c
Sequence 2, Application US/08891848
Patent No. 5953073
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5953073 yet assigned
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..6727
OTHER INFORMATION: /note="PET-11d-ANG-E6 fusion protein"
OTHER INFORMATION: sequence"
US-08-891-848-2

Query Match 100.0%; Score 24; DB 2; Length 6727;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaattcattgttgcagct 24
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Db 1530 CAAGAATTCTCATGTTGCAGCT 1507

RESULT 9
US-08-125-462-5/C
Sequence 5, Application US/08125462
Patent No. 5840840
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,462
FILING DATE: 22-SEP-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-110-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6799 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..6799
OTHER INFORMATION: /standard_name="PET-11d-E6-FB-EDN"

US-08-125-462-5

Query Match 100.0%; Score 24; DB 2; Length 6799;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaattcattgttgcagct 24
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Db 1602 CAAGAATTCTCATGTTGCAGCT 1579

RESULT 10
US-08-891-848-5/C
Sequence 5, Application US/08891848
Patent No. 595073
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 595073 yet assigned
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6799 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..6799
OTHER INFORMATION: /note="PET-11d-E6-FB-EDN fusion protein sequence"
OTHER INFORMATION: protein sequence"
US-08-891-848-5

Query Match 100.0%; Score 24; DB 2; Length 6799;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaattcattgttgcagct 24
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Db 1602 CAAGAATTCTCATGTTGCAGCT 1579

Fri Dec 14 09:21:22 2001

us-09-631-709-5.rni

Page 6

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RESULT 11
PCT-US96-05611A-12
Sequence 12, Application PC/TUS9605611A
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Leonardo, Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Matlis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8540 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Apex-3p Eukaryotic
PCT-US96-05611A-12
Query Match 100.0%; Score 24; DB 5; Length 8540;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 6105 CAAGAATTCATGTTTGACAGCT 6128
RESULT 12
PCT-US92-08258-6
Sequence 6, Application PC/TUS9208258
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC. and STATE OF OREGON BY AND
THROUGH THE OREGON STATE
```

```

TITLE OF INVENTION: PRODUCTION OF GPA NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08258
FILING DATE: 19920929
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean R.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/2253562
TELEFAX: 415/952-9881
FILING DATE:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8575 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-08258-6
Query Match 100.0%; Score 24; DB 5; Length 8575;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 caagaattcattgttgacagct 24
Db 8541 CAAGAATTCATGTTTGACAGCT 8564
RESULT 13
US-08-252-493C-8
Sequence 8, Application US/08252493C
Patent No. 5891645
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rotner, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matlis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,493C
FILING DATE: June 1, 1994
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8932 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Apex-3 Eukaryotic
DESCRIPTION: Expression Vector
US-08-252-493C-8

Query Match 100.0%; Score 24; DB 2; Length 8932;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgcagct 24
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Db 6497 CAAGAATTCATGTTGCAGCT 6520

RESULT 14
US-09-276-197-8
Sequence 8, Application US/09276197
Patent No. 6040428
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matlis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/252,493
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8932 base pairs
TYPE: Nucleic Acid

STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Apex-3 Eukaryotic
DESCRIPTION: Expression Vector
US-09-276-197-8

Query Match 100.0%; Score 24; DB 3; Length 8932;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgcagct 24
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Db 6497 CAAGAATTCATGTTGCAGCT 6520

RESULT 15
US-08-196-259-2
Sequence 2, Application US/08196259
Patent No. 5639596
GENERAL INFORMATION:
APPLICANT: BORNKAM, Georgy
APPLICANT: POLACK, Axel
TITLE OF INVENTION: DNA CONSTRUCT AND IN VITRO TEST FOR
TITLE OF INVENTION: DETECTING TUMOR PROMOTERS BY MEANS OF SAID DNA CONSTRUCT
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER, FRANK & SCHNEIDER
STREET: Suite 300 East - 1100 New York Ave., N.W.
CITY: Washington
STATE: DC

COUNTRY: US
ZIP: 20005-3955
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,259
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Spencer, George H.
REGISTRATION NUMBER: 18,038
REFERENCE/DOCKET NUMBER: FRK 0449
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 414-4000
TELEFAX: (202) 414-4040
TELEX: 64267
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11616 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/DE91/00652
FILING DATE: 16-AUG-1991
PUBLICATION DATE: 04-MAR-1993
US-08-196-259-2

Query Match 100.0%; Score 24; DB 1; Length 11616;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Fri Dec 14 09:21:22 2001

Db 11236 CAAGAATTCATCTTGACAGCT 11259

Search completed: December 13, 2001, 13:32:32
Job time: 346 sec

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:43:12 ; Search time 496.49 Seconds
(without alignments)
41.443 Million cell updates/sec

Title: US-09-631-709-5

Perfect score: 24

Sequence: 1 caagaattcattgttgcagact 24

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Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Maximum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	24	100.0	24	AAH46618	Primer #5. Synthe
3	24	100.0	29	AAH46618	Plasmid pUC.1 PCR
4	24	100.0	35	AAH46618	Uridase expression
5	24	100.0	35	AAH46618	PCR primer for con
6	24	100.0	3188	AAH46618	Sequence of plasmid
7	24	100.0	3276	AAH46618	Sequence of plasmid
8	24	100.0	3383	AAH46618	Sequence of plasmid
9	24	100.0	3427	AAH46618	Sequence of plasmid
10	24	100.0	3547	AAH46618	Plasmid sequence e
11	24	100.0	3557	AAH46618	Human pro-growth h

12	24	100.0	3621	7	AAH46618
13	24	100.0	3628	15	AAH46618
14	24	100.0	3854	17	AAH46618
15	24	100.0	3979	11	AAH46618
16	24	100.0	5552	21	AAH46618
17	24	100.0	6264	21	AAH46618
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19	24	100.0	6422	21	AAH46618
20	24	100.0	6623	14	AAH46618
21	24	100.0	6630	14	AAH46618
22	24	100.0	6652	21	AAH46618
23	24	100.0	6675	21	AAH46618
24	24	100.0	6727	20	AAH46618
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27	24	100.0	6799	20	AAH46618
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29	24	100.0	7013	21	AAH46618
30	24	100.0	7114	21	AAH46618
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33	24	100.0	8575	14	AAH46618
34	24	100.0	8932	20	AAH46618
35	24	100.0	8932	21	AAH46618
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37	24	100.0	10380	20	AAH46618
38	24	100.0	11265	19	AAH46618
39	24	100.0	11616	15	AAH46618
40	24	100.0	11616	15	AAH46618
41	24	100.0	16080	21	AAH46618
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44	24	100.0	20160	22	AAH46618
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ALIGNMENTS

RESULT 1	
AAH46618	standard; DNA; 24 BP.
XX	
XX	AAH46618:
XX	
XX	17-SEP-2001 (first entry)
XX	
XX	Synthetic oligonucleotide #21.
DE	
XX	Helicobacter pylori; alpha-1,2-fucosyltransferase;
KW	fucose-containing sugar production; Lewis antigen; ss.
KM	
XX	
XX	Synthetic.
OS	
XX	
XX	MO200146400-A1.
PN	
XX	
XX	28-JUN-2001.
PD	
XX	
XX	20-DEC-2000; 2000MO-JP09033.
PF	
XX	
XX	21-DEC-1999; 99JP-0362243.
PR	
XX	
XX	(KYOW) KYOWA HAKKO KOCYO KK.
PA	
XX	Endo T, Koizumi S, Tabata K, Ozaki A;
XX	
XX	WPI: 2001-418061/44.
DR	
XX	
XX	Modified alpha-1,2-fucosyltransferase gene and its expression product
PT	for efficient production of fucose-containing sugars such as Lewis
PT	antigen
XX	
PS	Example 3; Page 63; 69pp; Japanese.

Human pre-prolactin
Plasmid sequence e
Plasmid pSEC-cyt/c
Sequence of plasmid
pDIP/PyCSP.1 plasm
Destination vector
Destination vector
Destination vector
Sequence of circuli
Sequence of circuli
Destination vector
Destination vector
PET-11d-ANG-E6 DNA
Nucleic acid sequ
PET-11d-E6-FB-EDN
Nucleic acid sequ
Destination vector
Destination vector
Destination vector
Eukaryotic express
Vector PAPEX-3p.
Sequence of pHEB03
Apex-3 eukaryotic
Vector PAPEX-3. S
Nucleotide sequenc
Nucleotide sequenc
Plasmid pHEB03-DR-LU
Construct pHEB03-DR
DNA clone pCEK C1.
Nucleic acid sequ
Nucleic acid sequ
Nucleic acid sequ
Nucleic acid sequ

XX The invention relates to DNA encoding a modified form of the
CC alpha-1,2-fucosyltransferase of *Helicobacter pylori*. The
CC polycytosine sequence, the AAAAAG sequence and/or the number of TAA
CC repeats has been modified in the DNA sequence. The modified gene is
CC useful in the production of large amounts of fucose-containing
CC sugars, such as Lewis antigens for medicinal use. The present
CC sequence is an oligonucleotide provided in the specification.
XX
SQ Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24
Db 1 caagaattctcatgtttgacagct 24

RESULT 2

ID AAF62506 standard; DNA; 24 BP.
AC AAF62506;
XX
DT 08-MAY-2001 (first entry)
XX
DE Primer #5.
XX
KW Guanosine 5'-diphosphofucose; GDP-fucose;
KW Guanosine 5'-diphospho-4-keto-6-deoxymannose; GKDM; immunotherapy;
KW cardiovascular; infection; ss.
XX
OS Synthetic.
XX
PN EPI076096-A1.
XX
PD 14-FEB-2001.
XX
PF 10-AUG-2000; 2000EP-0117167.
XX
PR 10-AUG-1999; 99JP-0225889.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Koizumi S, Nagano H, Endo T, Tabata K, Ozaki A;
XX
DR WPI; 2001-193203/20.
XX
XX Producing guanosine 5'-diphosphofucose (GDP-fucose) useful as a
XX substrate of complex carbohydrates for immunotherapy comprises
XX employing microorganisms that convert guanosine
XX 5-diphospho-4-keto-6-deoxymannose to GDP-fucose
XX
PS Example 2; Page 12; 19pp; English.
XX
CC The present invention relates to producing guanosine
CC 5'-diphosphofucose (GDP-fucose) by employing an enzyme source
CC that is a culture broth of microorganisms. GDP-fucose is useful
CC as a synthetic substrate of complex carbohydrates that are useful
CC e.g. for immunotherapy for protection against cardiovascular
CC diseases, or infections by bacteria or viruses. Guanosine
CC 5'-diphospho-4-keto-6-deoxymannose (GKDM) is useful as
CC an intermediate for the production of GDP-fucose.
XX
SQ Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24
Db 1 caagaattctcatgtttgacagct 24

RESULT 3

ID AAF81198 standard; DNA; 29 BP.
AC AAF81198;
XX
DT 30-MAY-2001 (first entry)
XX
DE Plasmid pXC.1 PCR primer #1.
XX
KW Adenovirus; Ad; replication selective; tumour specific;
KW early gene 1A; E1A; cancer; restenosis; intimal proliferative disease;
KW primary pulmonary hypertension; cytostatic; hypotensive; vasotropic;
KW gene therapy; vaccine; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200123004-A1.
XX
PD 05-APR-2001.
XX
PF 02-OCT-2000; 2000WO-US27212.
XX
PR 30-SEP-1999; 99US-0157224.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Molnar-Kimber K, Toyozumi T;
XX
DR WPI; 2001-266112/27.
XX
XX Replication selective adenovirus mutant with improved selectivity for
XX tumor and hyperproliferative cells, for use in treating cancer and
XX hypertension, comprises a deactivated or crippled early gene promoter
XX
PS Example 1; Page 35; 56pp; English.
XX
CC The present sequence is a primer which was used in an example
CC illustrating an invention relating to a replication selective adenovirus
CC (Ad) mutant under the control of a tumour specific promoter. The Ad early
CC gene 1A (E1A) promoter has been deactivated or crippled to reduce
CC activity of the promoter to a lower level than wild-type Ad.
CC The adenovirus is useful for delivering a heterologous gene or gene
CC fragment, suicide gene or therapeutic gene, to a target cell. It is
CC also useful for treating a patient suffering from cancer, carcinoma,
CC sarcoma, neoplasm, leukemia, lymphoma or hyperproliferative cell
CC diseases, including restenosis, intimal proliferative disease and
CC primary pulmonary hypertension.
XX
SQ Sequence 29 BP; 8 A; 6 C; 4 G; 11 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24
Db 4 caagaattctcatgtttgacagct 27

RESULT 4

AAO40964
ID AAO40964 standard; DNA; 35 BP.
AC AAO40964;

```

XX 06-OCT-1993 (first entry)
DE Urlicase expression plasmid construction PCR primer.
XX Enzyme; uric acid; oxidation; allantoin; hydrogen peroxide; CO2;
XX production; blood; urine; determination; hair dye; dyeing;
KW polymerase chain reaction; 5'end; ss.
XX Synthetic.
XX EP545688-A.
XX 09-JUN-1993.
XX 02-DEC-1992; 92EP-0311004.
XX 04-DEC-1991; 91JP-0320525.
XX (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX Azuma M, Hasegawa M, Hashimoto Y, Ishino S, Iwata K, Teshiba S;
PI Yagasaki M, Yamaguchi K, Yano K, Yokoo Y;
XX WPI: 1993-184382/23.
XX DNA encoding uricase and process for producing uricase - used in
PT determining uric acid content of blood or urine and in hair
PT dyeing kits, etc.
XX Example; Page 14; 22pp; English.
XX The sequence is that of a 5'-end PCR primer, which was used in the
CC construction of an efficient uricase expression plasmid. It was
CC used to change the SD sequence of vector pIR53 into the SD sequence
CC of lacZ.
XX Sequence 35 BP; 9 A; 8 C; 5 G; 13 T; 0 other;
SQ

```

Query Match 100.0%; Score 24; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 caagaattcattgttgcagct 24
   ||||||||||||||||
Db 4 caagaattcattgttgcagct 27

```

RESULT 5
AAQ72263
ID AAQ72263 standard; DNA: 35 BP.
XX AAQ72263;
AC
XX 09-JUN-1995 (first entry)
DT
XX PCR primer for constructing lacZ-contg. plasmid pTL33.
DE
XX Cellulomonas flavigena SK-4; uricase; catalase katG gene; Kate gene;
KW inactivation; catalase-deficient bacterium; tryptophan promoter;
KW recombinant oxidase production; beta-galactosidase; ss.
XX Synthetic.
OS
XX JP06245762-A.
XX
XX 06-SEP-1994.
XX
XX 25-FEB-1993; 93JP-0036424.
XX
XX 25-FEB-1993; 93JP-0036424.
PR
XX

```

PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX WPI: 1994-321275/40.
XX Prepn. of oxidase - using catalase deficient Escherichia sp.
XX Example 1; Page 13; 15pp; Japanese.
XX
XX PCR primers AAQ72263-Q72264 were used in the construction of the
CC plasmid pTL33 which contains a trip-lac fusion. Plasmid pTL33 was
CC used in the construction of pUT118 for expression of the uricase
CC gene from Cellulomonas flavigena SK-4, placed downstream of the
CC tryptophan promoter. A catalase-deficient strain of bacteria was
CC prepared by substituting the katG and Kate genes with katG::CAT
CC and Kate::KAM fusion genes. The catalase-deficient E.coli are then
CC used as hosts for recombinant production of uricase.
XX
XX Sequence 35 BP; 9 A; 8 C; 5 G; 13 T; 0 other;
SQ

```

Query Match 100.0%; Score 24; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 caagaattcattgttgcagct 24
   ||||||||||||||||
Db 4 caagaattcattgttgcagct 27

```

RESULT 6
AAQ06310/C
ID AAQ06310 standard; DNA: 3188 BP.
XX AAQ06310;
AC
XX 29-JAN-1991 (first entry)
DT
XX Sequence of plasmid p79DBAM.
DE
XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
KW hypersensitivity; ds.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH LTR 279..335
FT /*tag= a
FT 497..502
FT /*tag= b
XX
XX EP393502-A.
XX
XX 24-OCT-1990.
XX
XX 11-APR-1990; 90EP-0106992.
XX
XX 19-APR-1989; 89EP-0810295.
XX
XX (HOFF) HOFFMANN-LA ROCHE AG.
PA Fountoulakis M, Garotta G, Stuber D;
PI WPI: 1990-322042/43.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune
XX diseases, chronic inflammations, etc.
XX
XX Disclosure; Fig 49; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment
CC of autoimmune disease, allograft transplant rejections, multiple
CC sclerosis, chronic inflammations and delayed hypersensitivity. It is
CC also useful in identifying IFN-gamma agonists and antagonists.

CC See also AA06301.

XX Sequence 3188 BP; 797 A; 774 C; 882 G; 735 T; 0 other;

SO

Query Match

Best Local Similarity 100.0%; Score 24; DB 11; Length 3188;
Matches 24; Conservative 0; Pred. No. 0.054; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctcatgtttgacagct 24
DB 642 CAAGATTCTCATGTTTGACAGCT 619

RESULT 7

AA06311/c
ID AA06311 standard; DNA: 3276 BP.

AC AA06311;

DT 29-JAN-1991 (first entry)

DB Sequence of plasmid p238BGL.

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT LTR 279..242

FT CDS 243..426

FT Sig-peptide 243..405

FT /tag= b

FT /label= S.P.1

FT /tag= d

FT polyA_signal

XX EP393502-A.

XX 24-OCT-1990.

XX 11-APR-1990; 90EP-0106992.

XX 19-APR-1989; 89EP-0810295.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Fountoulakis M, Garotta G, Stubber D;

XX WPI; 1990-322042/43.

XX P-PSDB; AAR07065.

XX Soluble interferon-gamma receptors - for treating auto-immune

XX diseases, chronic inflammations, etc.

XX Disclosure; Fig 51; 174pp; English.

XX IFN-gamma is a therapeutically active agent in the treatment

XX of autoimmune disease, allograft transplant rejections, multiple

XX sclerosis, chronic inflammations and delayed hypersensitivity. It is

XX also useful in identifying IFN-gamma agonists and antagonists.

XX See also AA06301.

XX Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 other;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

OY 1 caagaattcctcatgtttgacagct 24

DB 730 CAAGATTCTCATGTTTGACAGCT 707

RESULT 8

AA06309/c
ID AA06309 standard; DNA: 3383 BP.

AC AA06309;

DT 29-JAN-1991 (first entry)

DB Sequence of plasmid p76BGL.

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

XX hypersensitivity; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT LTR 279..504

FT CDS 505..540

FT /tag= b

FT /tag= c

FT polyA_signal

XX EP393502-A.

XX 24-OCT-1990.

XX 11-APR-1990; 90EP-0106992.

XX 19-APR-1989; 89EP-0810295.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Fountoulakis M, Garotta G, Stubber D;

XX WPI; 1990-322042/43.

XX P-PSDB; AAR07065.

XX Soluble interferon-gamma receptors - for treating auto-immune

XX diseases, chronic inflammations, etc.

XX Disclosure; Fig 47; 174pp; English.

XX IFN-gamma is a therapeutically active agent in the treatment

XX of autoimmune disease, allograft transplant rejections, multiple

XX sclerosis, chronic inflammations and delayed hypersensitivity. It is

XX also useful in identifying IFN-gamma agonists and antagonists.

XX See also AA06301.

XX Sequence 3383 BP; 838 A; 828 C; 929 G; 788 T; 0 other;

XX

XX

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XX

XX

```

XX Sequence of plasmid p267BGL.
DE
XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
KM hypersensitivity; ds.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT LTR 279..492
FT CDS /*tag= a
FT /*tag= a
FT /*tag= b
FT Sig-peptide 493..585
FT /*tag= b
FT /*tag= c
FT polyA_signal /*label= S.p.2
FT 736..741
FT /*tag= d
XX
XX EP393502-A.
XX
XX 24-OCT-1990.
XX
XX 11-APR-1990: 90EP-0106992.
XX
XX 19-APR-1989: 89EP-0810295.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Fountoulakis M, Garotta G, Stuber D;
XX
XX WPI: 1990-322042/43.
XX
XX P-PSDB; AAR07067.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune
PT diseases, chronic inflammations, etc.
XX
XX Disclosure; Fig 59; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment
CC of autoimmune disease, allograft transplant rejections, multiple
CC sclerosis, chronic inflammations and delayed hypersensitivity. It is
CC also useful in identifying IFN-gamma agonists and antagonists.
CC See also AAQ06301.
XX
XX Sequence 3427 BP; 846 A; 840 C; 942 G; 799 T; 0 other;
SQ

```

Query Match 100.0%; Score 24; DB 11; Length 3427;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgcagct 24
 |||
 Db 881 CAAGAATTCATCTGTGACAGCT 858

RESULT 10
 AAN60846
 ID AAN60846 standard; DNA: 3547 BP.
 XX
 XX AAN60846;
 XX
 XX 24-OCT-1991 (first entry)
 XX
 XX Plasmid sequence encoding bovine pre-growth hormone.
 XX
 XX E.coli; pre-prolactin; bGH; bPRL; ds.
 XX
 XX Bos taurus.
 XX
 XX JP61202691-A.
 XX

```

PD 08-SEP-1986.
XX
XX 04-MAR-1985; 85JP-0042406.
XX
XX 04-MAR-1985; 85JP-0042406.
XX
XX (NAKA/) NAKAJIMA K.
XX
XX WPI: 1986-276389/42.
XX
XX Plasmid(s) contg. ampicillin resistant genes - for amplification
PT of bovine growth hormone and prolactin genes.
XX
XX Disclosure; Table 1-18; 13pp; Japanese.
XX
XX The bovine pre-growth hormone encoding sequence is derived from
CC pituitary tissue. The plasmids carry an amp resistance gene and,
CC and may be expressed by an E.coli host in an ampicillin medium
CC for efficient and large scale production of the hormone.
XX
XX Sequence 3547 BP; 901 A; 902 C; 912 G; 832 T; 0 other;
SQ

```

Query Match 100.0%; Score 24; DB 7; Length 3547;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcattgttgcagct 24
 |||
 Db 3513 caagaattcattgttgcagct 3536

RESULT 11
 AAN60801
 ID AAN60801 standard; DNA: 3557 BP.
 XX
 XX AAN60801;
 XX
 XX 24-OCT-1991 (first entry)
 XX
 XX Human pro-growth hormone.
 DE
 XX Pituitary gland; E.coli; ds.
 XX
 XX Homo sapiens.
 OS
 XX JP61202689-A.
 XX
 XX 08-SEP-1986.
 XX
 XX 04-MAR-1985; 85JP-0042404.
 XX
 XX 04-MAR-1985; 85JP-0042404.
 XX
 XX (NAKA/) NAKAJIMA K.
 XX
 XX WPI: 1986-276387/42.
 XX
 XX Plasmid for amplification of human growth hormone gene - derived
PT from human pituitary gland tissue.
XX
XX Disclosure; Table 1-9; 9pp; Japanese.
XX
XX Sequence is derived from human pituitary gland tissue, and allows
CC pro-growth hormone to be produced by a circular plasmid carrying an
CC amp resistance gene, from a transformed E.coli expression system in
CC an ampicillin containing medium.
XX See also J61202690.
XX
XX Sequence 3557 BP; 927 A; 902 C; 897 G; 831 T; 0 other;
SQ

Query Match 100.0%; Score 24; DB 7; Length 3557;

Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctcattgttgcagct 24
|||||
Db 3523 caagaattcctcattgttgcagct 3546

RESULT 12

AAN60847
ID AAN60847 standard; DNA; 3621 BP.

AC AAN60847;

DT 24-OCT-1991 (first entry)

DE Human pre-prolactin gene.

KW Pituitary gland; E.coli; ds.

OS Homo sapiens.

PN JP61202690-A.

PD 08-SEP-1986.

PF 04-MAR-1985; 85JP-0042405.

PR 04-MAR-1985; 85JP-0042405.

PA (NAKA/) NAKAJIMA K.

DR WPI; 1986-276389/42.

XX Plasmid for amplification of the human prolactin gene - derived from human pituitary tissue and cultivated in ampicillin contg.

PT medium to obtain a PBR 322 ampicillin resistant gene.

PS Disclosure; Table 1-9; 9pp; Japanese.

CC Sequence is derived from human pituitary gland tissue, and allows pre-prolactin to be produced by a circular plasmid carrying an amp resistance gene, from a transformed E.coli expression system in an CC ampicillin containing medium.
CC See also JP61202689.

SQ Sequence 3621 BP; 969 A; 882 C; 894 G; 876 T; 0 other;

Query Match 100.0%; Score 24; DB 7; Length 3621;
Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctcattgttgcagct 24
|||||
Db 3587 caagaattcctcattgttgcagct 3610

RESULT 13

AAN60848
ID AAN60848 standard; DNA; 3628 BP.

AC AAN60848;

DT 24-OCT-1991 (first entry)

DE Plasmid sequence encoding bovine pre-prolactin hormone.

KW E.coli; growth hormone; bGH; bPRL; ds.

OS Bos taurus.

PN JP61202691-A.

XX 08-SEP-1986.
PD 04-MAR-1985; 85JP-0042406.

PF 04-MAR-1985; 85JP-0042406.

PR 04-MAR-1985; 85JP-0042406.

PA (NAKA/) NAKAJIMA K.

DR WPI; 1986-276389/42.

PT Plasmid(s) contg. ampicillin resistant genes - for amplification of bovine growth hormone and prolactin genes.

PS Disclosure; Table 1-18; 13pp; Japanese.

CC The bovine pre-prolactin hormone encoding sequence is derived from CC pituitary tissue. The plasmids carry an amp resistance gene and, CC and may be expressed by an E.coli host in an ampicillin medium for efficient and large scale production of the hormone.

SQ Sequence 3628 BP; 965 A; 873 C; 901 G; 889 T; 0 other;

Query Match 100.0%; Score 24; DB 7; Length 3628;
Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctcattgttgcagct 24
|||||
Db 3594 caagaattcctcattgttgcagct 3617

RESULT 14

AA067221
ID AA067221 standard; DNA; 3854 BP.

AC AA067221;

DT 24-MAR-1995 (first entry)

DE Plasmid pSEC-cyt/c DNA encoding pre-apo-protein.

KW Plasmid pSEC-cyt/c; vector; holo-protein; pre-apo-protein; protein synthesis; Escherichia coli; cytoplasm cytochrome; ss.

OS Synthetic.

Key Location/Qualifiers
FH 396..454

FT misc_feature /tag= a

FT promoter /label= polylinker-site

FT misc_feature /tag= b

FT misc_feature /label= pho-promoter

FT sig_peptide /tag= c

FT misc_feature /label= Shine-Dalgarno-sequence

FT misc_feature /tag= d

FT misc_feature /note= "alkaline phosphatase signal peptide"

FT misc_feature /tag= f

FT misc_feature /note= "soluble core of cytochrome-b5"

FT misc_feature /tag= g

FT misc_feature /note= "tail of cytochrome-b5"

PN WO9417191-A.

PD 04-AUG-1994.

PF 27-JAN-1994; 94WO-GB00161.

XX 27-JAN-1993; 93GB-0001553.
 XX (UYWA-) UNIV COLLEGE WALES.
 PA Kaderbhal MA;
 XX WPI: 1994-264104/32.
 DR P-PSDB; AAR57733.
 XX
 PT Genetic precursor unit causing periplasmic translocation of
 PT pre-apo-protein - for processing the halo-protein, useful in
 PT protein synthesis, assay of signal peptidase and identification
 PT of its inhibitors
 XX
 PS Claim 10; Fig.5; 32pp; English.
 XX
 CC This plasmid contains a DNA sequence encoding the pre-form of an apo-
 CC protein such that the pre-apo-protein is translocated from a
 CC cytoplasmic cell region to a periplasmic region where formation of
 CC process apo-protein and conversion to halo-protein to occur. The
 CC DNA encoded in this plasmid is expressed in the cytoplasm of E. coli,
 CC especially TB-1 and M830-1. The apo-protein is a cytoplasmic
 CC cytochrome, especially having a soluble core domain of cytochrome-b5
 CC of liver endoplasmic reticulum. The sequence also encodes an E.
 CC coli alkaline phosphatase signal peptide.
 XX
 SQ Sequence 3854 BP; 1005 A; 938 C; 965 G; 946 T; 0 other;

Query Match 100.0%; Score 24; DB 15; Length 3854;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 caagaattctcatgtttgacagct 24
 |||||
 Db 2689 caagaattctcatgtttgacagct 2712

RESULT 15
 AAQ06312/c
 ID AAQ06312 standard; DNA; 3979 BP.
 XX
 AC AAQ06312;
 XX
 DT 29-JAN-1991 (first entry)
 XX
 DE Sequence of plasmid p264BGL.
 XX
 KM IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 KW hypersensitivity; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT LTR 279..242 /*tag= a
 FT CDS 243..426 /*tag= b
 FT Sig-peptide 243..405 /*tag= c
 FT polyA_signal /label= S.P.1
 FT 1288..1292 /*tag= d
 XX
 XX EP393502-A.
 XX
 XX 24-OCT-1990.
 XX
 XX 11-APR-1990; 90EP-0106992.
 XX
 XX 19-APR-1989; 89EP-0810295.
 XX

PA (HOFF) HOFFMANN-LA ROCHE AG.
 XX
 XX Fountoulakis M, Garotta G, Stuber D;
 XX WPI: 1990-322042/43.
 DR P-PSDB; AAR07066.
 XX
 PT Soluble interferon-gamma receptors - for treating auto-immune
 PT diseases, chronic inflammations, etc.
 XX
 PS Disclosure; Fig 55; 174pp; English.
 XX
 CC IFN-gamma is a therapeutically active agent in the treatment
 CC of autoimmune disease, allograft transplant rejections, multiple
 CC sclerosis, chronic inflammations and delayed hypersensitivity. It is
 CC also useful in identifying IFN-gamma agonists and antagonists.
 CC See also AAQ06301.
 XX
 SQ Sequence 3979 BP; 947 A; 987 C; 1113 G; 932 T; 0 other;

Query Match 100.0%; Score 24; DB 11; Length 3979;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 caagaattctcatgtttgacagct 24
 |||||
 Db 1433 CAAGAATTCTCATGTTTGACAGCT 1410

Search completed: December 13, 2001, 15:43:13
 Job time: 8187 sec

Fri Dec 14 09:21:22 2001

us-09-631-709-5.rng

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:35:42 ; Search time 1854.2 Seconds
(without alignments) 213.533 Million cell updates/sec

Title: US-09-631-709-5
Sequence: 1 caagaattctatgttgcagcgt 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_ov:*
21: em_or:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8 SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6 AX137661	AX137661 Sequence
2	24	100.0	35	6 E06705	E06705 PCR primer.
3	24	100.0	41	12 SYN5188V	K02384 Plasmid vec
4	24	100.0	43	12 SYN52421	K02386 Plasmid vec
5	24	100.0	55	6 A31312	A31312 DNA fragmen
6	24	100.0	55	6 A31313	A31313 DNA fragmen
7	24	100.0	55	6 I50064	I50064 Sequence 1
8	24	100.0	62	1 E00952PRQ	K01791 E.coli tet
9	24	100.0	200	12 SYN313FR	M10197 Plasmid pBR
10	24	100.0	1764	6 E08771	E08771 DNA encodin
11	24	100.0	1797	6 I03265	I03265 Sequence 4
12	24	100.0	2256	6 E01322	E01322 DNA transfe
13	24	100.0	2256	6 E08770	E08770 DNA encodin
14	24	100.0	3300	1 AFO19744	AFO19744 Agrobacte
15	24	100.0	3387	6 E00974	E00974 cDNA encodi
16	24	100.0	3468	6 E00954	E00954 Plasmid for
17	24	100.0	3477	6 E00952	E00952 Plasmid DNA
18	24	100.0	3541	6 E00953	E00953 Plasmid for
19	24	100.0	3549	6 E00955	E00955 Plasmid for
20	24	100.0	3773	12 SYNPT551V	L09154 pMT551 expr
21	24	100.0	3809	12 SYNPT511V	L09153 pMT511 expr
22	24	100.0	3918	6 AR077142	AR077142 Sequence
23	24	100.0	4151	1 RCFD0E	Y11304 R. capsulatu
24	24	100.0	4753	1 BTF6407	AJ006407 Bacillus
25	24	100.0	4892	12 XXU02429	U02429 Cloning vec
26	24	100.0	4896	12 XXU13868	U13868 pSVL clonin
27	24	100.0	4985	12 AF147464	AF147464 T7 expres
28	24	100.0	5066	12 SCU40398	U40398 Synthetic c
29	24	100.0	5228	12 XXU25059	U25059 Cloning vec
30	24	100.0	5345	12 SYNPUR288V	L09147 PUR288 clon
31	24	100.0	5347	12 SYNPUR289V	L09148 PUR289 clon
32	24	100.0	5348	12 SYNPUR291V	L09150 PUR291 clon
33	24	100.0	5349	12 SYNPUR292V	L09151 PUR292 clon
34	24	100.0	5351	12 SYNPUR290V	L09146 PUR278 clon
35	24	100.0	5353	12 SYNPUR290V	L09149 PUR290 clon
36	24	100.0	6433	12 AF020539	AF020539 Shuttle v
37	24	100.0	6623	6 AR068550	AR068550 Sequence
38	24	100.0	6630	6 A23373	A23373 Artificial
39	24	100.0	6630	6 AR068551	AR068551 Sequence
40	24	100.0	6727	6 AR060673	AR060673 Sequence
41	24	100.0	6727	6 AR074430	AR074430 Sequence
42	24	100.0	6799	6 AR060676	AR060676 Sequence
43	24	100.0	6799	6 AR074433	AR074433 Sequence
44	24	100.0	8097	12 SCU46780	U46780 Synthetic c
45	24	100.0	8932	6 AR069417	AR069417 Sequence

ALIGNMENTS

RESULT 1
AX137661
LOCUS AX137661 DNA 24 bp
DEFINITION Sequence 5 from Patent EP1076096.
ACCESSION AX137661
VERSION AX137661.1 GI:14273846
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 24)
AUTHORS Koizumi,S., Nagano,H., Endo,T., Tabata,K. and Ozaki,A.
TITLE Process for producing gdp-fucose
JOURNAL Patent: EP 1076096-A 5 14-FEB-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
LOCATION/Qualifiers

FEATURES
Source
1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA"

BASE COUNT 7 a 5 c 4 g 8 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24
DB 1 CAAGAATTCTCATGTGACAGCT 24

RESULT 2

LOCUS E06705 35 bp DNA PAT 29-SEP-1997
DEFINITION PCR primer.
ACCESSION E06705 1 GI:2174867
VERSION JP 1994038766-A/7.
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 35)
AUTHORS Tagasaki, M., Ishino, S., Iwata, K., Azuma, M., Teshiba, S.,
Hasegawa, M., Yamaguchi, K., Yano, K., Yokoo, Y. and Hashimoto, Y.
TITLE URICASE GENE AND PRODUCTION OF URICASE
JOURNAL Patent: JP 1994038766-A 7 15-FEB-1994;
KYOWA HAKKO KOGYO CO LTD
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1994038766-A/7
PD 15-FEB-1994
PE 04-DEC-1991 JP 1991320525
PI YAGASAKI MAKOTO, ISHINO SHUICHI, IWATA KAZUHISA, PI AZUMA
MASAYUKI,
PI TESHIBA SADAOK, HASEGAWA MASARU, YAMAGUCHI KAZUO, YANO KEIICHI,
PI YOKOO YOSHIMARU, HASHIMOTO YUKIO
PC C12N15/53, C12N1/20, C12N1/21, C12N9/06, (C12N15/53, C12N1:01), PC
(C12N1/20,
PC C12N1:01), (C12N1/21, C12N1:19), (C12N9/06, C12N1:19), (C12N9/06,
PC C12N1:01);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;

FEATURES

source 1..35
/organism="synthetic construct"
/db_xref="taxon:32630" 5 g 13 t
BASE COUNT 9 a 8 c 5 g
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24
DB 4 CAAGAATTCTCATGTGACAGCT 27

RESULT 3

LOCUS SYN188V 41 bp DNA SYN 27-APR-1993
DEFINITION Plasmid vector pBR3188 derived from deletion of 12 bp of pBR322,
destroying Tc-promoter.
ACCESSION K02384
VERSION K02384.1 GI:2093117
KEYWORDS drug resistance protein; mutational analysis; promoter region;
tetacycline resistance.
SOURCE pBR322 DNA, clone pBR 188.

ORGANISM unidentified cloning vector
artificial sequence; vectors.

REFERENCE 1 (bases 1 to 41)
AUTHORS Savochkina, L.P., Retchinsky, V.O. and Beabealashvili, R.S.
TITLE Stability of cloned promoter-containing fragments
JOURNAL Mol. Gen. Genet. 189, 142-147 (1983)
MEDLINE 83218507

COMMENT [1] inserted strong promoters from T7 and lambda into pBR322
derived promoter-probe vectors. The inserted promoters, which
occurred in dissimilar environments, served as promoters for the
pBR322 tetacycline resistance operon. Promoter strength was
measured by Tc resistance. Plasmids containing T7 A2 promoters
appeared to confer less Tc resistance than those containing A3
promoters.

FEATURES Location/Qualifiers
source 1..41
/organism="unidentified cloning vector"
/db_xref="taxon:45196" 8 g 14 t
BASE COUNT 9 a 10 c 8 g
ORIGIN 10 bp upstream of EcoRI site.

Query Match 100.0%; Score 24; DB 12; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24
DB 7 CAAGAATTCTCATGTGACAGCT 30

RESULT 4

LOCUS SYN2421 43 bp DNA SYN 27-APR-1993
DEFINITION Plasmid vector pBR3242 derived from insertion of lac UV5 promoter-
operator region into pBR322; region 5' to UV5 insertion.
ACCESSION K02386
VERSION K02386.1 GI:209320
KEYWORDS drug resistance protein; mutational analysis; promoter region;
tetacycline resistance.
SEGMENT 1 of 2
SOURCE pBR322 DNA, clone pBR 242.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 43)
AUTHORS Savochkina, L.P., Retchinsky, V.O. and Beabealashvili, R.S.
TITLE Stability of cloned promoter-containing fragments
JOURNAL Mol. Gen. Genet. 189, 142-147 (1983)
MEDLINE 83218507

COMMENT [1] inserted strong promoters from T7 and lambda into pBR322
derived promoter-probe vectors. The inserted promoters, which
occurred in dissimilar environments, served as promoters for the
pBR322 tetacycline resistance operon. Promoter strength was
measured by Tc resistance. Plasmids containing T7 A2 promoters
appeared to confer less Tc resistance than those containing A3
promoters.

FEATURES Location/Qualifiers
source 1..43
/organism="synthetic construct"
/db_xref="taxon:32630" 6 g 16 t
BASE COUNT 11 a 10 c 6 g
ORIGIN 10 bp upstream of EcoRI site.

Query Match 100.0%; Score 24; DB 12; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattctcatgtttgacagct 24
DB 7 CAAGAATTCTCATGTGACAGCT 30

RESULT 5
LOCUS A31312 55 bp DNA PAT 03-NOV-1995
DEFINITION DNA fragment (PBR322 restriction fragment) from patent WO9012321.
ACCESSION A31312
VERSION A31312.1 GI:1249336
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 55)
AUTHORS
TITLE HALOGENATED DNA LIGAND RADIOSENSITISERS FOR CANCER THERAPY
JOURNAL Patent: WO 9012321-A 1 18-OCT-1990;
FEATURES Location/Qualifiers
1..55
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 13 a 13 c 10 g 19 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctatgtttacagct 24
|||||
Db 17 CAAGAATTCATGTTGACAGCT 40

RESULT 6
LOCUS A31313 55 bp DNA PAT 03-NOV-1995
DEFINITION DNA fragment (PBR322 restriction fragment) from patent WO9012321.
ACCESSION A31313
VERSION A31313.1 GI:1247258
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 55)
AUTHORS
TITLE HALOGENATED DNA LIGAND RADIOSENSITISERS FOR CANCER THERAPY
JOURNAL Patent: WO 9012321-A 2 18-OCT-1990;
FEATURES Location/Qualifiers
1..55
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 19 a 10 c 13 g 13 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctatgtttacagct 24
|||||
Db 39 CAAGAATTCATGTTGACAGCT 16

RESULT 7
LOCUS 150064 55 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5641764.
ACCESSION 150064
VERSION 150064.1 GI:2472284
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 55)
TITLE Unclassified.

AUTHORS Martin, R. Francis and Kelly, D. Patterson.
TITLE Halogenated DNA ligand radiosensitizers for cancer therapy
JOURNAL Patent: US 5641764 A 1 24-JUN-1997;
FEATURES Location/Qualifiers
1..55
/organism="unknown"
BASE COUNT 13 a 13 c 10 g 19 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctatgtttacagct 24
|||||
Db 17 CAAGAATTCATGTTGACAGCT 40

RESULT 8
LOCUS ECOTETPRO 62 bp DNA BCT 26-APR-1993
DEFINITION E. coli tet promoter region.
ACCESSION K01791
VERSION K01791.1 GI:147933
KEYWORDS mutational analysis; promoter region.
SOURCE E. coli DNA.
ORGANISM Escherichia coli
REFERENCE 1 (bases 1 to 62)
AUTHORS Russell, D. R. and Bennett, G. N.
TITLE Construction and analysis of in vivo activity of E. coli promoter
JOURNAL hybrids and promoter mutants that alter the -35 to -10 spacing
MEDLINE Gene 20, 231-243 (1982)
COMMENT [1] examines the efficiency of gene expression in E. coli if the distance between the -35 and -10 regions is changed. When two bases are inserted increasing the span to 19 there is no gene expression and when 1 base is inserted (as in tet 18 bp), expression is reduced to 50% of normal.
FEATURES Location/Qualifiers
1..62
/organism="Escherichia coli"
/db_xref="taxon:562"
-35-signal 20..25
-10-signal 43..48
BASE COUNT 17 a 11 c 10 g 24 t
ORIGIN 41 bp upstream of HindIII site.

Query Match 100.0%; Score 24; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcctatgtttacagct 24
|||||
Db 5 CAAGAATTCATGTTGACAGCT 28

RESULT 9
LOCUS SYN313FR/c 200 bp DNA SYN 09-APR-1996
DEFINITION Plasmid PBR313 DNA fragment.
ACCESSION M10197 M28278
VERSION M10197.1 GI:207771
KEYWORDS
SOURCE Cloning vector (sub-species Cloning vector PBR313) DNA.
ORGANISM unidentified cloning vector
REFERENCE 1 (bases 1 to 200)
AUTHORS Wilkins, R. J.
TITLE Selective binding of actinomycin D and distamycin A to DNA

JOURNAL Nucleic Acids Res. 10 (22), 7273-7282 (1982)
MEDLINE 83116954
FEATURES Location/Qualifiers
source 1..200
/organism="unidentified cloning vector"
/sub_species="Cloning vector pBR313"
/db_xref="taxon:45196"

BASE COUNT 58 a 33 c 43 g 66 t
ORIGIN 31 bp upstream of EcoRI site.

Query Match 100.0%; Score 24; DB 12; Length 200;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcctcattgttgacagct 24
DB 39 CAAGAATTCATGTTGACAGCT 16

RESULT 10
LOCUS E08771 1764 bp DNA PAT
DEFINITION DNA encoding hybrid protein of beta-glucuronidase and protein A.
ACCESSION E08771
VERSION E08771.1 GI:2176883
KEYWORDS JP 1995051086-A/2.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1764)
AUTHORS Jiyon,E.P. and Argusiu,A.
TITLE HYBRID PROTEIN PRODUCED BY ULTRA-HIGH DEGREE PROCARYOTE EXPRESSION SYSTEM
JOURNAL Patent: JP 1995051086-A 2 28-FEB-1995;
REPLIGEN CORP

COMMENT OS None
OC Artificial sequences.
PN JP 1995051086-A/2
PD 28-FEB-1995
PF 07-MAR-1986 JP 1994069101
PI JIYON ERU PAMMA, ARGUSIU ANIRTONISU
PC C12P21/02.C07K19/00,C12N1/21,C12N15/09,(C12P21/02,C12R1:19),
PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..1764
FT FT /clone="pcBS" /organism="Artificial sequences" FT
FT mat_peptide 502..1764
FT /product="Protein A-like hybrid protein".

FEATURES Location/Qualifiers
source 1..1764
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 639 a 373 c 337 g 415 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcctcattgttgacagct 24
DB 1747 CAAGAATTCATGTTGACAGCT 1724

RESULT 11
103265/c

LOCUS 103265 1797 bp ss-DNA PAT
DEFINITION Sequence 4 from Patent US 488280.
ACCESSION 103265
VERSION 103265.1 GI:270747
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1797)
AUTHORS Palmer,J.L. and Anilionis,A.
TITLE Hybrid proteins produced by an ultrahigh prokaryotic expression
JOURNAL Patent: US 488280-A 4 19-DEC-1989;
Repligen Corporation;
Cambridge, MA
FEATURES Location/Qualifiers
source 1..1797
/organism="unknown"
BASE COUNT 670 a 374 c 373 g 380 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 1797;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caagaattcctcattgttgacagct 24
DB 1777 CAAGAATTCATGTTGACAGCT 1754

RESULT 12
LOCUS E01322 2256 bp DNA PAT
DEFINITION DNA transfer vector encoding hybrid protein.
ACCESSION E01322
VERSION E01322.1 GI:2169581
KEYWORDS JP 1987207297-A/1.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2256)
AUTHORS Jiyon,E.P. and Argusiu,A.
TITLE HYBRID PROTEIN PREPARED BY ULTRAHIGH PROCARYOTIC EXPRESSION SYSTEM
JOURNAL Patent: JP 1987207297-A 1 11-SEP-1987;
REPLIGEN CORP

COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1987207297-A/1
PD 11-SEP-1987
PF 07-MAR-1986 JP 1986048770
PI JIYON ERU PAMMA, ARGUSIU ANIRTONISU
PC C07K13/00,A61K35/74,A61K37/00,C07H21/04,C12N1/20,C12N15/00, PC
C12P21/02,
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: NO;
FH Key Location/Qualifiers
FT misc-feature 1..2256
FT FT /note="DNA transfer vector which encodes FT
FT hybrid protein of
FT beta-glucuronidase and A2 protein".
FT Location/Qualifiers
source 1..2256
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 767 a 478 c 474 g 537 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2256;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgacagct 24
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 Db 2239 CAAGAATTCATGTTGACAGCT 2216

RESULT 13
 E08770/c 2256 bp DNA PAT 29-SEP-1997
 LOCUS DNA encoding hybrid protein of beta-glucuronidase and protein A.
 DEFINITION E08770
 ACCESSION E08770
 VERSION E08770.1 GI:2176882
 KEYWORDS JP 1995051086-A/1.
 SOURCE unclassified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 2256)
 AUTHORS Jiyon, E.P. and Arugisu, A.
 TITLE HYBRID PROTEIN PRODUCED BY ULTRA-HIGH DEGREE PROCARYOTE EXPRESSION SYSTEM
 JOURNAL Patent: JP 1995051086-A 1 28-FEB-1995;
 REPLICEN CORP
 OS None
 OC Artificial sequences.
 PN JP 1995051086-A/1
 PD 28-FEB-1995
 PF 07-MAR-1986 JP 1994069101
 PI JIYON ERU PAMAMA, ARUGISU ANIRIONISU
 PC C12P21/02,C07K19/00,C12N1/21,C12N15/09,(C12P21/02,C12R1:19),
 PC (C12N1/21,
 PC C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..2256
 FT /clone='pBg9', /organism='Artificial sequences' FT
 FT mat_peptide 502..2256
 FT /product='Protein A-like hybrid protein'.
 FEATURES
 source Location/Qualifiers
 1..2256
 /organism='unidentified'
 /db_xref='taxon:32644'
 BASE COUNT 767 a 478 c 474 g 537 t
 ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2256;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgacagct 24
 ||||||||||||||||||
 Db 2239 CAAGAATTCATGTTGACAGCT 2216

RESULT 14
 AF019744/c 3300 bp DNA BCT 02-APR-1998
 LOCUS Agrobacterium tumefaciens plasmid pGV 3850:1003 T-DNA, left border.
 DEFINITION AF019744
 ACCESSION AF019744
 VERSION AF019744.1 GI:3004665
 KEYWORDS
 SOURCE Agrobacterium tumefaciens.
 ORGANISM Agrobacterium tumefaciens
 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 Rhizobiaceae; Rhizobium.
 REFERENCE 1 (bases 1 to 3300)
 AUTHORS Feldmann, K.A.

TITLE T-DNA insertion mutagenesis in Arabidopsis: seed infection/transformation
 JOURNAL Methods in Arabidopsis Research 10, 274-289 (1992)
 REFERENCE 2 (bases 1 to 3300)
 AUTHORS Tisler, C.P., Zambryski, P. and Feldmann, K.A.
 TITLE Complete 3 kb left border sequence of the 3850:1003 T-DNA
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 3300)
 AUTHORS Tisler, C.P., Zambryski, P. and Feldmann, K.A.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-1997) Plant Sciences, University of Arizona,
 Forbes Building 303, Tucson, AZ 85721, USA
 FEATURES
 source Location/Qualifiers
 1..3300
 /organism='Agrobacterium tumefaciens'
 /strain='C58 C1 R1f'
 /db_xref='taxon:358'
 /plasmid='pGV 3850:1003'
 misc_feature 1..3300
 /note='T-DNA left border'
 BASE COUNT 901 a 679 c 769 g 932 t 19 others
 ORIGIN

Query Match 100.0%; Score 24; DB 1; Length 3300;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 caagaattcattgttgacagct 24
 ||||||||||||||||||
 Db 3052 CAAGAATTCATGTTGACAGCT 3029

RESULT 15
 E00974 3387 bp RNA PAT 29-SEP-1997
 LOCUS cDNA encoding human growth factor 20K.
 DEFINITION E00974
 ACCESSION E00974
 VERSION E00974.1 GI:2169235
 KEYWORDS JP 1986224988-A/1.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3387)
 AUTHORS Nakajima, K. and Nagai, J.
 TITLE RECOMBINANT PLASMID OF ESCHERICHIA COLI FOR AMPLIFYING
 JOURNAL COMPLEMENTARY DNA OF HUMAN GROWTH HORMONE 20K
 Patent: JP 1986224988-A 1 06-OCT-1986;
 NAKAJIMA KUNIO
 COMMENT
 OS Human
 PN JP 1986224988-A/1
 PD 06-OCT-1986
 PF 29-MAR-1985 JP 1985066208
 PI NAKAJIMA KUNIO, NAGAI JUN
 PC C12N15/00//C12P21/02,(C12N15/00,C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: tissue=intestine;
 FEATURES
 source Location/Qualifiers
 1..3387
 /organism='Homo sapiens'
 /db_xref='taxon:9606'
 BASE COUNT 855 a 880 c 842 g 810 t
 ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 3387;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Dec 14 09:21:21 2001

us-09-631-709-5.rge

Page 6

Oy 1 caagaattctcatgtttgacagct 24
|||||
Db 3353 CAAGAATTCTCATGTTCACAGCT 3376

Search completed: December 13, 2001, 15:35:43
Job time: 7737 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:03:33 ; Search time 5599.23 Seconds
(without alignments)
38.383 Million cell updates/sec

Title: US-09-631-709-2
Perfect score: 20
Sequence: 1 gagctgactgggttcgaagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: qd_est1:*
11: qd_est2:*
12: qd_hic:*
13: qd_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	184	11	BG874396
2	20	100.0	185	11	BG874387
3	20	100.0	186	11	BG874391
4	20	100.0	194	11	BG874395
5	20	100.0	201	11	BG874379
6	20	100.0	202	11	BG874517
7	20	100.0	203	11	BG874381
8	20	100.0	203	11	BG874511
9	20	100.0	205	11	BG874394
10	20	100.0	206	10	AW994158
11	20	100.0	219	11	BG874516
12	20	100.0	220	11	BG874514

13	20	100.0	221	11	BG874513	BG874513	QV4-BN003
14	20	100.0	221	10	BG878325	BG878325	QV2-ST029
15	20	100.0	258	10	AV036275	AV036275	AV036275
16	20	100.0	349	11	BG063262	BG063262	H3005A05-
17	20	100.0	378	11	BG874522	BG874522	QV4-BN003
18	20	100.0	390	10	AA966183	AA966183	V4a04a1.f
19	20	100.0	469	13	AC640463	AC640463	927P1-13C
20	20	100.0	486	10	AA111347	AA111347	mos3f05.r
21	20	100.0	491	13	P859R	P859R	AL390539
22	20	100.0	507	10	AL499935	AL499935	AL499935
23	20	100.0	519	10	AM539899	AM539899	CO125H03-
24	20	100.0	588	13	A2124374	A2124374	SB122-T7
25	20	100.0	612	10	AL499952	AL499952	AL499952
26	20	100.0	699	10	AL500397	AL500397	AL500397
27	20	100.0	699	10	AL500414	AL500414	AL500414
28	20	100.0	700	10	AL500060	AL500060	AL500060
29	20	100.0	703	10	AG012834	AG012834	AG012834
30	20	100.0	705	13	AG012835	AG012835	Homo sapi
31	20	100.0	713	13	AG012836	AG012836	Homo sapi
32	20	100.0	720	13	AG000789	AG000789	Homo sapi
33	20	100.0	722	13	AG000790	AG000790	Homo sapi
34	20	100.0	723	13	AG000764	AG000764	Homo sapi
35	20	100.0	725	13	AG000765	AG000765	Homo sapi
36	20	100.0	1716	12	AK005545	AK005545	Mus muscu
37	20	100.0	1958	12	AK005492	AK005492	Mus muscu
38	18.4	92.0	367	11	BI285916	BI285916	UI-R-CX0S
39	18.4	92.0	387	10	AA491025	AA491025	UI-M-BH3-
40	18.4	92.0	437	10	AA490684	AA490684	UI-M-BH3-
41	18.4	92.0	660	11	BI285964	BI285964	UI-R-CX0S
42	18.4	92.0	759	11	BI285886	BI285886	UI-R-CX0S
43	18.4	92.0	763	11	BI284457	BI284457	UI-R-CX0S
44	18.4	92.0	813	11	BG518807	BG518807	602578104
45	18.4	92.0	900	11	BF168996	BF168996	601775266

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BG874396	BG874396	QV4-BN0025-010200-097-f12 BN0025	BG874396	BG874396.1	GI:14251327	EST.	human.
REFERENCE	AUTHORS	DIAS Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Bala,G.S., Simpson,D.H., Brunsstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.					
TITLE	JOURNAL MEDLINE COMMENT	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
		Contact: Simpson A.J.G.					
		Laboratory of Cancer Genetics					
		Ludwig Institute for Cancer Research					
		Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil					
		Tel: +55-11-2704922					
		Fax: +55-11-2707001					
		Email: asimpson@ludwig.org.br					
		This sequence was derived from the RAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL					
		(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QV4-BN0025-010200-097-f12et3=2000-02-01et4=1)					
		Seq primer: puc 18 forward					

High quality sequence start: 9
High quality sequence stop: 184.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0025"
/dev_stage="Adult"

/note="Organ: breast,normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 43 a 55 c 54 g 32 t
ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 184;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
|||||
DB 127 GAGCTGACTGGTTGAAGC 146

RESULT 2

LOCUS BG874387 185 bp mRNA EST 30-MAY-2001
DEFINITION QV4-BN0025-010200-097-c12 BN0025 Homo sapiens CDNA, mRNA sequence.
ACCESSION BG874387
VERSION BG874387.1 GI:14251318
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 185)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES
source 1. 185
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0025"
/dev_stage="Adult"
/note="Organ: breast,normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 43 a 55 c 54 g 32 t
ORIGIN

Query Match

100.0%; Score 20; DB 11; Length 186;

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 41 a 58 c 54 g 32 t
ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 185;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
|||||
DB 128 GAGCTGACTGGTTGAAGC 147

RESULT 3

LOCUS BG874391 186 bp mRNA EST 30-MAY-2001
DEFINITION QV4-BN0025-010200-097-e07 BN0025 Homo sapiens CDNA, mRNA sequence.
ACCESSION BG874391
VERSION BG874391.1 GI:14251322
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 186)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES
source 1. 186
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0025"
/dev_stage="Adult"
/note="Organ: breast,normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 43 a 55 c 54 g 34 t
ORIGIN

BG8/43/9/c

REFERENCE 1 (bases 1 to 202)

1 (bases 1 to 202)

AUTHORS
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.G.

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL MEDLINE COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
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 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpsoneludwig.org.br

FEATURES
 source
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV4-BN0036-140
 200-097-010&tl3=2000-02-01&tl4=1)
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 High quality sequence stop: 202.
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 1..202
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 /db_xref="taxon:9606"
 /clone_lib="BN0036"
 /dev_stage="Adult"
 /note="Organ: breast-normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
 46 a 60 c 58 g 38 t

ORIGIN
 100.0%; Score 20; DB 11; Length 202;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 gagctgactgggttaagc 20
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 Db 145 GAGCTGACTGGGTTGAGGC 164

RESULT 7
 BG874381 203 bp mRNA EST 30-MAY-2001
 LOCUS QV4-BN0025-010200-097-a10 BN0025 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG874381
 ACCESSION BG874381
 VERSION BG874381.1 GI:14251312
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 203)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.G.

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL MEDLINE COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpsoneludwig.org.br

FEATURES
 source
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV4-BN0025-010
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 High quality sequence start: 26
 High quality sequence stop: 203.
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 /clone_lib="BN0025"
 /dev_stage="Adult"
 /note="Organ: breast-normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
 32 a 60 c 61 g 50 t

ORIGIN
 100.0%; Score 20; DB 11; Length 203;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 gagctgactgggttaagc 20
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 Db 42 GAGCTGACTGGGTTGAGGC 23

RESULT 8
 BG874511 203 bp mRNA EST 30-MAY-2001
 LOCUS QV4-BN0036-140200-104-a12 BN0036 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG874511
 ACCESSION BG874511
 VERSION BG874511.1 GI:14251442
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 203)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.G.

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL MEDLINE COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

CONTACT: Simpson A.J.G.
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 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpsoneludwig.org.br

FEATURES
 source
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.php?l=6&t2=QV4-BN0036-140200-104-a12&t3=2000-02-14&t4=1>)

Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 203.

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 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
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 DB 149 GAGCTGACTGGTTGAAGC 168

RESULT 11

LOCUS BC874516 219 bp mRNA EST 30-MAY-2001
 DEFINITION OY4-BN0036-140200-104-c01 BN0036 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BC874516
 VERSION BC874516.1 GI:14251447
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS 1 (bases 1 to 219)
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-QV4-BN0036-140
 200-104-c01&t3=2000-02-14&t4=1)
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 High quality sequence stop: 219.

FEATURES

source

1..219
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BN0036"
 /dev_stage="Adult"
 /note="Organ: breast,normal; Vector: puc18; Site:1: Sma1;
 Site:2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 52 a 67 c 63 g 37 t
 ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 219;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
 ||||||||||||||||
 DB 162 GAGCTGACTGGTTGAAGC 181

RESULT 12

LOCUS BC874514 220 bp mRNA EST 30-MAY-2001
 DEFINITION OY4-BN0036-140200-104-c02 BN0036 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BC874514
 VERSION BC874514.1 GI:14251445
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS 1 (bases 1 to 220)
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-QV4-BN0036-140
 200-104-c02&t3=2000-02-14&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 5
 High quality sequence stop: 220.

FEATURES

source

1..220
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BN0036"
 /dev_stage="Adult"
 /note="Organ: breast,normal; Vector: puc18; Site:1: Sma1;
 Site:2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 52 a 68 c 63 g 37 t
 ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 220;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
 ||||||||||||||||
 DB 163 GAGCTGACTGGTTGAAGC 182

RESULT 13

LOCUS BC874513 221 bp mRNA EST 30-MAY-2001
 DEFINITION OY4-BN0036-140200-104-c01 BN0036 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BC874513
 VERSION BC874513.1 GI:14251444
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 221)
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-QV4-BN0036-140
 200-104-c01ct3-2000-02-14&4=1)
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 /dev_stage="Adult"
 /note="Organ: breast normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT
 52 a 68 c 63 g 38 t
 ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 221;
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 164 GAGCTGACTGCGTTGAAGC 183

RESULT 14
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 LOCUS QV2-ST0298-240200-063-g01 ST0298 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG878325
 ACCESSION BG878325.1 GI:14255415
 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 221)
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
 MEDLINE
 COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-QV2-ST0298-240
 200-063-g01ct3-2000-02-24&4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 221.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ST0298"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT
 53 a 68 c 62 g 38 t
 ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 221;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 gaagctgactggtgaagc 20
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 Db 164 GAGCTGACTGCGTTGAAGC 183

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 LOCUS AV036275 Mus musculus adult C57BL/6J placenta Mus musculus cDNA
 DEFINITION AV036275
 ACCESSION AV036275.1 GI:4855940
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 258)
 Carninci, P., Shibata, K., Ozawa, Y., Kono, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Natsuna, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomioka, N., Muramatsu, M., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Watanabe, S., Okazaki, Y. and Hayashizaki, Y.
 RIKEN Mouse ESTs
 Unpublished (1999)
 Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@tc.riken.go.jp
 Thermostabilization and thermoactivation of thermostable enzymes by

trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

source

1. 258
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1600017M18"
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/tissue_type="placenta"
/dev_stage="adult"

BASE COUNT 67 a 63 c 60 g 68 t
ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;
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Db 120 GAGCTGACTGGGTGAAGGC 101

Search completed: December 13, 2001, 15:03:35
Job time: 5809 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 19:14:03 ; Search time 2658.89 Seconds
(without alignments)
10.708 Million cell updates/sec

Title: US-09-631-709-2

Perfect score: 20

Sequence: 1 gagctgactggtgaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 959380 seqs, 71176033 residues

Total number of hits satisfying chosen parameters: 1918760

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	5438	US-09-689-914-25	Sequence 25, Appl
C 3	20	100.0	5438	US-09-689-916-25	Sequence 25, Appl
C 4	20	100.0	5495	US-09-891-685A-4	Sequence 4, Appl
C 5	20	100.0	5556	US-09-891-685A-2	Sequence 2, Appl
C 6	20	100.0	5658	US-09-689-913-10	Sequence 10, Appl
C 7	20	100.0	5658	US-09-689-916-10	Sequence 10, Appl
C 8	20	100.0	5822	US-09-891-685A-8	Sequence 8, Appl
C 9	20	100.0	6046	US-09-891-685A-15	Sequence 15, Appl
C 10	20	100.0	6166	US-09-611-451-51	Sequence 51, Appl
C 11	20	100.0	6269	US-09-891-685A-9	Sequence 9, Appl
C 12	20	100.0	6299	US-09-891-685A-10	Sequence 10, Appl
C 13	20	100.0	6301	US-09-891-685A-6	Sequence 6, Appl
C 14	20	100.0	7714	US-09-276-820A-26	Sequence 26, Appl
C 15	20	100.0	8031	US-09-850-716A-254	Sequence 3, Appl
C 16	20	100.0	8592	US-09-666-238-3	Sequence 3, Appl
C 17	20	100.0	12980	US-09-963-433-5	Sequence 5, Appl
C 18	20	100.0	413	US-09-933-524A-80149	Sequence 80149, A
C 19	20	100.0	419	US-09-933-524A-26906	Sequence 26906, A
C 20	20	100.0	440	US-09-933-524A-98104	Sequence 98104, A
C 21	20	100.0	475	US-09-933-524A-11298	Sequence 11298, A
C 22	20	100.0	475	US-09-898-888A-3832	Sequence 3832, Ap
C 23	20	100.0	559	US-09-922-279A-1645	Sequence 1645, Ap
C 24	20	100.0	1102	US-09-965-529-68	Sequence 68, Appl
C 25	20	100.0	1215	US-09-719-961-1	Sequence 1, Appl

C 27	16.4	82.0	3395	US-09-898-888A-14401	Sequence 14401, A
C 28	16.4	82.0	25905	US-09-815-264-58164	Sequence 58164, A
C 29	15.8	79.0	259	US-09-983-402-1660	Sequence 1660, Ap
C 30	15.8	79.0	592	US-09-922-279A-1036	Sequence 1036, Ap
C 31	15.8	79.0	954	US-09-880-729-1	Sequence 1, Appl
C 32	15.8	79.0	1501	US-09-815-264-23442	Sequence 23442, A
C 33	15.8	79.0	3437	US-09-895-211-3	Sequence 3, Appl
C 34	15.8	79.0	13345	US-09-815-264-61249	Sequence 61249, A
C 35	15.8	79.0	14139	US-09-922-279A-4	Sequence 4, Appl
C 36	15.8	79.0	20128	US-09-815-264-62997	Sequence 62997, A
C 37	15.8	79.0	25995	US-09-815-264-80136	Sequence 80136, A
C 38	15.8	79.0	56178	US-09-815-264-83271	Sequence 83271, A
C 39	15.4	77.0	264	US-09-985-678-163782	Sequence 163782, A
C 40	15.4	77.0	272	US-09-985-678-292739	Sequence 292739, A
C 41	15.4	77.0	364	US-09-985-678-244601	Sequence 244601, A
C 42	15.4	77.0	1109	US-09-760-446A-934	Sequence 934, App
C 43	15.4	77.0	5154	US-09-815-264-90237	Sequence 90237, A
C 44	15.4	77.0	25978	US-09-815-264-65273	Sequence 65273, A
C 45	15.2	76.0	211	US-09-388-906A-19325	Sequence 19325, A

ALIGNMENTS

RESULT 1
US-09-689-913-25/c
Sequence 25, Application US/09689913

GENERAL INFORMATION:
APPLICANT: Iztutsu, Hiroshi
APPLICANT: Obara, Kazuhiko
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
TITLE OF INVENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUR
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
TITLE OF INVENTION: PNEUMONIAE GENE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,913
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,326
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995

Fri Dec 14 09:21:16 2001

us-09-631-709-2.inpu

Page 2

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 669-8864/9741
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 5438 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid; Plasmid
US-09-689-913-25

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 5438;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaactgactgggtgaagc 20
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DB 1694 GAGCTGACTGGGTGAAGC 1675

RESULT 2
US-09-689-914-25/c
Sequence 25, Application US/09689914
GENERAL INFORMATION:
APPLICANT: Izutsu, Hiroshi
APPLICANT: Obara, Kazuhiko
APPLICANT: Matsumoto, Akira
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
TITLE OF INVENTION: ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
TITLE OF INVENTION: OF ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,914
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,326
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 669-8864/9741
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 5438 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid; Plasmid
US-09-689-914-25

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 5438;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1694 GAGCTGACTGGGTGAAGC 1675

RESULT 3
US-09-689-916-25/c
Sequence 25, Application US/09689916
GENERAL INFORMATION:
APPLICANT: Izutsu, Hiroshi
APPLICANT: Obara, Kazuhiko
APPLICANT: Matsumoto, Akira
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
TITLE OF INVENTION: ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
TITLE OF INVENTION: OF ANTIODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,916
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,326
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 5438 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid; Plasmid
US-09-689-916-25

Query Match 100.0%; Score 20; DB 6; Length 5438;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttggaagc 20
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Db 1694 GAGCTGACTGGGTGGAAGC 1675

RESULT 4
US-09-891-685A-4
Sequence 4, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
TITLE OF INVENTION: natural nucleosides and modified analogues thereof
FILE REFERENCE: 99PC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: M198A002792
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 5495
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Plasmid
NAME/KEY: gene
LOCATION: (231)..(960)
OTHER INFORMATION: deod
NAME/KEY: gene
LOCATION: (1423)..(2822)
OTHER INFORMATION: tetracycline resistance
US-09-891-685A-4

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2162 gagctgactgggttggaagc 2181

RESULT 5
US-09-891-685A-2
Sequence 2, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
TITLE OF INVENTION: natural nucleosides and modified analogues thereof
FILE REFERENCE: 99PC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: M198A002792
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 5556
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Plasmid
NAME/KEY: gene
LOCATION: (243)..(1021)
OTHER INFORMATION: udp
NAME/KEY: gene
LOCATION: (1483)..(2883)
OTHER INFORMATION: tetracycline resistance
US-09-891-685A-2

Query Match 100.0%; Score 20; DB 6; Length 5556;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttggaagc 20
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Db 2223 gagctgactgggttggaagc 2242

RESULT 6
US-09-689-913-10/C
Sequence 10, Application US/09689913
GENERAL INFORMATION:
APPLICANT: Izutsu, Hiroshi
APPLICANT: Odara, Kazuhiko
APPLICANT: Matsumoto, Akira
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES, DNAS CODING
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, TRANSFORMA
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
TITLE OF INVENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
TITLE OF INVENTION: OF ANTIBODY, METHOD AND AGENTS FOR DIAGNOSIS OF CHLAMYDIA
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
TITLE OF INVENTION: PNEUMONIAE GENE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Fri Dec 14 09:21:16 2001

us-09-631-709-2.inpu

Page 4

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,913
FILING DATE:
CLASSIFICATION:
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APPLICATION NUMBER: 08/809,326
FILING DATE:
PRIOR APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426-043-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5658 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid; Plasmid
US-09-689-913-10

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DB 1914 GAGCTGACTGGGTGAAGC 1895

RESULT 7
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Sequence 10, Application US/09689914
GENERAL INFORMATION:
APPLICANT: Izutsu, Hiroshi
APPLICANT: Obata, Kazuhiko
APPLICANT: Matsumoto, Akira
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMANTS
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION OF
TITLE OF INVENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
TITLE OF INVENTION: OF ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREMENT
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND/OR
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/689,914
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,326
FILING DATE:
PRIOR APPLICATION NUMBER: JP 106006/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106008/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106009/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106010/95
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 106011/95
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7426-043-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5658 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid; Plasmid
US-09-689-914-10

Query Match
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1914 GAGCTGACTGGGTGAAGC 1895

RESULT 8
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Sequence 10, Application US/09689916
GENERAL INFORMATION:
APPLICANT: Izutsu, Hiroshi
APPLICANT: Obata, Kazuhiko
APPLICANT: Matsumoto, Akira
TITLE OF INVENTION: CHLAMYDIA PNEUMONIAE ANTIGENIC POLYPEPTIDES,
TITLE OF INVENTION: FUSED PROTEINS CONTAINING THE POLYPEPTIDES, DNAS CODING
TITLE OF INVENTION: THEREFOR, RECOMBINANT VECTORS CARRYING THE DNAS, TRANSFORMA
TITLE OF INVENTION: CONTAINING THE RECOMBINANT VECTORS, METHOD FOR PRODUCTION O
TITLE OF INVENTION: ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
TITLE OF INVENTION: OF ANTIBODY, METHOD AND REAGENTS FOR DETECTION AND/OR MEASUREM
TITLE OF INVENTION: PNEUMONIAE INFECTIONS, PROBES AND PRIMERS FOR DETECTION AND
TITLE OF INVENTION: MEASUREMENT OF CHLAMYDIA PNEUMONIAE GENE, AND METHOD AND
TITLE OF INVENTION: REAGENTS FOR DETECTION AND/OR MEASUREMENT OF CHLAMYDIA

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; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/09/689,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,326
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 106006/95
; FILING DATE: 28-APR-1995
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; APPLICATION NUMBER: JP 106010/95
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 106011/95
; FILING DATE: 28-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7426-043-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid: Plasmid
; US-09-689-916-10

Query Match          100.0%; Score 20; DB 6; Length 5658;
Best Local Similarity 100.0%; Pred. No. 2.2;
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Db 1914 GAGCTGACTGCTGGAAGC 1895

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US-09-891-685A-8
; Sequence 8, Application US/09891685A
; GENERAL INFORMATION:
; APPLICANT: NORPHARMA SPA
; TITLE OF INVENTION: Recombinant bacterial strains for the production of
; TITLE OF INVENTION: natural nucleosides and modified analogues thereof
; FILE REFERENCE: 99DC26E
; CURRENT APPLICATION NUMBER: US/09/891,685A
; CURRENT FILING DATE: 2001-06-25
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; PRIOR APPLICATION NUMBER: M198A002792
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 15
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; SEQ ID NO 8
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pgm716 with
; OTHER INFORMATION: deletion of HpaI fragment
US-09-891-685A-8

Query Match          100.0%; Score 20; DB 6; Length 5822;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2489 gagctgactggttggaagc 2508

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US-09-891-685A-15
; Sequence 15, Application US/09891685A
; GENERAL INFORMATION:
; APPLICANT: NORPHARMA SPA
; TITLE OF INVENTION: Recombinant bacterial strains for the production of
; TITLE OF INVENTION: natural nucleosides and modified analogues thereof
; FILE REFERENCE: 99DC26E
; CURRENT APPLICATION NUMBER: US/09/891,685A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: M198A002792
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.1
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: udp and deod
; OTHER INFORMATION: cloned downstream plac promoter
US-09-891-685A-15

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; Sequence 51, Application US/09611451
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; BURTON, Dennis R.
; LERNER, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel
; STREET: 10550 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
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us-09-631-709-2.inp

Page 6

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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0
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APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIORITY APPLICATION DATA:
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FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,153
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784,8297
TELEFAX: (619) 784,8399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-611-451-51
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DB 656 GAGCTGACTGGTTGAAGC 637
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RESULT 12
US-09-891-685A-9
Sequence 9, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
FILE REFERENCE: 99DC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
CURRENT FILING DATE: 2001-06-25
PRIORITY APPLICATION NUMBER: M198A002792
PRIORITY FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 9
LENGTH: 6269
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: udp and deod
OTHER INFORMATION: cloned in pUC18 so to create a fusion between the
US-09-891-685A-9
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US-09-891-685A-10
Sequence 10, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
FILE REFERENCE: 99DC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
CURRENT FILING DATE: 2001-06-25
PRIORITY APPLICATION NUMBER: M198A002792
PRIORITY FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 10
LENGTH: 6299
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: udp and deod
OTHER INFORMATION: cloned in pUC18 so to create a fusion between the
US-09-891-685A-10
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Sequence 6, Application US/09891685A
GENERAL INFORMATION:
APPLICANT: NORPHARMA SPA
TITLE OF INVENTION: Recombinant bacterial strains for the production of
FILE REFERENCE: 99DC26E
CURRENT APPLICATION NUMBER: US/09/891,685A
CURRENT FILING DATE: 2001-06-25
PRIORITY APPLICATION NUMBER: M198A002792
PRIORITY FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 6301
TYPE: DNA
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OTHER INFORMATION: Description of Artificial Sequence: Plasmid
LOCATION: (243)..(1021)
NAME/KEY: gene
LOCATION: (1037)..(1766)
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NAME/KEY: gene
LOCATION: (2229)..(3628)
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Best Local Similarity 100.0%; Score 20; DB 6; Length 6301;
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; Sequence 26, Application US/09276820A
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/276,820A
; CURRENT FILING DATE: 1999-03-26
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
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; PRIOR FILING DATE: 1999-02-19
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0, Gapext 1.0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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2	20	100.0	169	US-08-781-969-2722	Sequence 2722, Ap
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4	20	100.0	169	US-08-956-171B-2722	Sequence 2722, Ap
5	20	100.0	169	US-08-956-171C-2722	Sequence 2722, Ap
6	20	100.0	185	US-09-834-366-32199	Sequence 32199, A
7	20	100.0	185	US-09-197-873-32199	Sequence 32199, A
8	20	100.0	243	US-06-182-316-11146	Sequence 11146, A
9	20	100.0	294	US-08-808-443A-2457	Sequence 2457, Ap
10	20	100.0	294	US-08-880-314-881	Sequence 881, Ap
11	20	100.0	294	US-06-012-233-2457	Sequence 2457, Ap
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15	20	100.0	794	US-06-233-942-36	Sequence 36, Appl
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34	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
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36	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
37	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
38	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
39	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
40	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
41	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
42	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap
43	20	100.0	807	US-09-764-891-5573	Sequence 5573, Ap

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C 42 20 100.0 2562 22
C 43 20 100.0 2607 1
C 44 20 100.0 2607 1
C 45 20 100.0 2607 1

Sequence 3188, Ap
Sequence 10418, A
Sequence 24075, A
Sequence 2884, Ap

ALIGNMENTS

RESULT 1
US-09-631-709-2
; Sequence 2, Application US/09631709
; GENERAL INFORMATION:
; APPLICANT: KIOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: PROCESS FOR PRODUCING GDP-FUCOSE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/631,709
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-631-709-2

Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
Db 1 gagctgactgggttgaagc 20

RESULT 2
US-08-781-986A-2722
; Sequence 2722, Application US/08781986A
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; OPERATING SYSTEM: HP Vectra 486/33
; SOFTWARE: MSDOS version 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2722:
; SEQUENCE CHARACTERISTICS:

LENGTH: 169 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-2722

Query Match 100.0%; Score 20; DB 11; Length 169;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
Db 112 GAGCTGACTGGGTGAAGC 131

RESULT 3
US-08-956-171-2722
; Sequence 2722, Application US/08956171
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; OPERATING SYSTEM: HP Vectra 486/33
; SOFTWARE: MSDOS version 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2722:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-956-171-2722

Query Match 100.0%; Score 20; DB 13; Length 169;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gagctgactgggttgaagc 20
Db 112 GAGCTGACTGGGTGAAGC 131

RESULT 4
US-08-956-171B-2722
; Sequence 2722, Application US/08956171B
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GIL H. Choi


```

; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171B
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 2722:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2722:
US-08-956-171B-2722

Query Match          100.0%; Score 20; DB 13; Length 169;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
   |||
Db 112 GAGCTGACTGGGTGAAGC 131

RESULT 5
US-08-956-171C-2722
; Sequence 2722, Application US/08956171C
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GILL H. CHOI
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171C
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 2722:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2722:
US-08-956-171C-2722

Query Match          100.0%; Score 20; DB 13; Length 169;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
   |||
Db 112 GAGCTGACTGGGTGAAGC 131

RESULT 6
US-09-834-366-32199
; Sequence 32199, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81 US2, REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 32199
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-834-366-32199

Query Match          100.0%; Score 20; DB 31; Length 185;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
   |||
Db 10 gagctgactgggttgaagc 29

RESULT 7
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US-60-197-873-32199
; Sequence 32199
; GENERAL INFORMATION:
; APPLICANT: Rejzlin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Duma, Milne Edwards, Jean Baptiste
; APPLICANT: Giordano, Jean Yves
; TITLE OF INVENTION: SRS and Encoded Human Proteins.
; FILE REFERENCE: 81 US PRO
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 32199
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-197-873-32199
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Query Match
Best Local Similarity 100.0%; Score 20; DB 52; Length 185;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactgggttgaagc 20
DB 10 gagctgactgggttgaagc 29
```

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RESULT 8
US-60-182-316-11146
; Sequence 11146, Application US/60182316
; GENERAL INFORMATION:
; APPLICANT: Curtis, Anne L.
; APPLICANT: Lagace, Robert E.
; APPLICANT: Klingler, Tod M.
; APPLICANT: Scuve, Laura L.
; TITLE OF INVENTION: CPG Island Polynucleotides
; FILE REFERENCE: PX-0003 P
; CURRENT APPLICATION NUMBER: US/60/182,316
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 14,630
; SOFTWARE: IREL Program
; SEQ ID NO 11146
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: CPG_991027_B15_masked_fa.Contig36197
US-60-182-316-11146
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```
Query Match
Best Local Similarity 100.0%; Score 20; DB 51; Length 243;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactgggttgaagc 20
DB 178 gagctgactgggttgaagc 197
```

```
RESULT 9
US-08-808-443A-2457/C
; Sequence 2457, Application US/08808443A
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerdion, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
```

```
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM HUMAN
NUMBER OF SEQUENCES: 9111
CORRESPONDENCE ADDRESS: 3111
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/08/808,443A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION: 536
NAME: FISHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD 0117P
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (415) 852-0555
FAX: (415) 852-1195
INFORMATION FOR SEQ ID NO 2457:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 831577
US-08-808-443A-2457
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 294;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactgggttgaagc 20
DB 21 GAGCTGACTGGGTGAAGC 2
```

```
RESULT 10
US-08-880-314-881/C
; Sequence 881, Application US/08880314
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerdion, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
NUMBER OF SEQUENCES: 4685
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,314
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/020,415
FILING DATE: JUNE 24, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025,817
FILING DATE: SEPTEMBER 5, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,443
FILING DATE: FEBRUARY 26, 1997
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0197 US
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 881:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 831577
US-08-880-314-881

Query Match 100.0%; Score 20; DB 12; Length 294;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20
|||||
DB 21 GAGCTGACTGGTTGAAGC 2

RESULT 11
US-60-012-233-2457/c
Sequence 2457, Application US/60012233
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Ted M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM HUMAN
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/012,233

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD 0117P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 852-0195
INFORMATION FOR SEQ ID NO: 2457:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 831577
US-60-012-233-2457

Query Match 100.0%; Score 20; DB 34; Length 294;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20
|||||
DB 21 GAGCTGACTGGTTGAAGC 2

RESULT 12
US-60-233-942-25/c
Sequence 25, Application US/60233942
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHASE II
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
FILE REFERENCE: C1000825
CURRENT APPLICATION NUMBER: US/60/233,942
NUMBER OF SEQ ID NOS: 210
CURRENT FILING DATE: 2000-09-18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 689
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(689)
OTHER INFORMATION: n = A,T,C or G
US-60-233-942-25

Query Match 100.0%; Score 20; DB 56; Length 689;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgaagc 20
|||||
DB 48 GAGCTGACTGGTTGAAGC 29

RESULT 13
US-60-233-942-36/c
Sequence 36, Application US/60233942
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHASE II
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
FILE REFERENCE: C1000825
CURRENT APPLICATION NUMBER: US/60/233,942

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; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 751
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(751)
; OTHER INFORMATION: n = A,T,C or G
US-60-233-942-36

Query Match
Best Local Similarity 100.0%; Score 20; DB 56; Length 751;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactgggttgaagc 20
DB 313 GAGCTGACTGGGTGAAGCC 294

RESULT 14
PCT-US01-01339-5573
; Sequence 5573, Application PC/TUS0101339
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5573
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-01339-5573

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 794;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactgggttgaagc 20
DB 756 gagctgactgggttgaagc 775

RESULT 15
PCT-US01-01339-5603
; Sequence 5603, Application PC/TUS0101339
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5603
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-01339-5603

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 794;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactgggttgaagc 20

DB 756 gagctgactgggttgaagc 775
Search completed: December 13, 2001, 18:29:31
Job time: 18165 sec

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 13:29:57 ; Search time 176.03 Seconds
(without alignments)
25.732 Million cell updates/sec

Title: US-09-631-709-2
Perfect score: 20
Sequence: 1 gacgtactggtggtgaagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	41	3	US-08-973-965-1
2	20	100.0	92	3	US-08-973-965-3
3	20	100.0	95	3	US-08-973-965-39
4	20	100.0	710	3	US-09-098-287A-5
5	20	100.0	1130	2	US-08-613-965-1
6	20	100.0	1130	2	US-08-918-966-1
7	20	100.0	1130	3	US-08-921-655-1
8	20	100.0	1140	1	US-08-218-303-15
9	20	100.0	1140	2	US-08-338-793D-60
10	20	100.0	3301	2	US-08-447-430A-42
11	20	100.0	3423	2	US-08-447-430A-40
12	20	100.0	3474	2	US-08-447-430A-41
13	20	100.0	3474	2	US-08-318-837-10
14	20	100.0	4009	2	US-08-500-860A-2
15	20	100.0	4245	2	US-08-929-967-4
16	20	100.0	4309	5	PCT-US91-02954-11
17	20	100.0	4593	4	US-08-801-344-1
18	20	100.0	4593	4	US-09-498-599-1
19	20	100.0	4619	1	US-08-450-257-20
20	20	100.0	4619	1	US-08-450-246-20
21	20	100.0	4619	1	US-08-450-246-20
22	20	100.0	4819	1	US-08-450-098-20
23	20	100.0	4819	1	US-08-451-233-20
24	20	100.0	4819	1	US-08-450-236-20
25	20	100.0	4910	1	US-08-450-257-11
26	20	100.0	4910	1	US-08-450-246-11
27	20	100.0	4910	1	US-08-450-098-11
	20	100.0	4910	1	US-08-451-233-11

28	20	100.0	4910	1	US-08-450-236-11	Sequence 11, Appl
29	20	100.0	4977	1	US-08-450-257-14	Sequence 14, Appl
30	20	100.0	4977	1	US-08-450-257-17	Sequence 14, Appl
31	20	100.0	4977	1	US-08-450-246-14	Sequence 17, Appl
32	20	100.0	4977	1	US-08-450-246-17	Sequence 14, Appl
33	20	100.0	4977	1	US-08-450-098-14	Sequence 14, Appl
34	20	100.0	4977	1	US-08-450-098-17	Sequence 17, Appl
35	20	100.0	4977	1	US-08-451-233-14	Sequence 14, Appl
36	20	100.0	4977	1	US-08-451-233-17	Sequence 17, Appl
37	20	100.0	4977	1	US-08-450-236-17	Sequence 14, Appl
38	20	100.0	4977	1	US-08-450-236-17	Sequence 17, Appl
39	20	100.0	4990	3	US-08-776-511-1	Sequence 1, Appl
40	20	100.0	5098	1	US-08-450-257-10	Sequence 10, Appl
41	20	100.0	5098	1	US-08-450-246-10	Sequence 10, Appl
42	20	100.0	5098	1	US-08-450-098-10	Sequence 10, Appl
43	20	100.0	5098	1	US-08-451-233-10	Sequence 10, Appl
44	20	100.0	5098	1	US-08-450-236-10	Sequence 10, Appl
45	20	100.0	5115	3	US-08-825-852-19	Sequence 19, Appl

ALIGNMENTS

```

RESULT 1
US-08-973-965-1/c
; Sequence 1, Application US/08973965
; Patent No. 6033881
; GENERAL INFORMATION:
; APPLICANT: HIMMELER, Gottfried
; APPLICANT: SCHLEDERER, Thomas
; TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF
; FILE REFERENCE: 030560-055
; CURRENT APPLICATION NUMBER: US/08-973,965
; EARLIER FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: AT A 1007/95
; EARLIER FILING DATE: 1995-06-13
; EARLIER APPLICATION NUMBER: PCT/AT96/00106
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 41
; TYPE: DNA
; ORGANISM: synthetic construct
US-08-973-965-1

Query Match          100.0%; Score 20; DB 3; Length 41;
Best local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gacgtactggtggtgaagc 20
|||||
DB 23 GACGTACTGCTGTTGAAGGC 4

RESULT 2
US-08-973-965-3/c
; Sequence 3, Application US/08973965
; Patent No. 6033881
; GENERAL INFORMATION:
; APPLICANT: HIMMELER, Gottfried
; APPLICANT: SCHLEDERER, Thomas
; TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF
; FILE REFERENCE: 030560-055
; CURRENT APPLICATION NUMBER: US/08-973,965
; EARLIER FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: AT A 1007/95
; EARLIER FILING DATE: 1995-06-13
; EARLIER APPLICATION NUMBER: PCT/AT96/00106
; EARLIER FILING DATE: 1996-06-13

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Page 2

NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 92
TYPE: DNA
ORGANISM: synthetic construct
US-08-973-965-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 92;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgagc 20
DB 23 GAGCTGACTGGTTGAGGC 4

RESULT 3
US-08-973-965-39/c
Sequence 39, Application US/08973965
Patent No. 6033881
GENERAL INFORMATION:
APPLICANT: HIMLER, Gottfried
APPLICANT: SCHLEDERER, Thomas
TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF
FILE REFERENCE: 030560-055
CURRENT APPLICATION NUMBER: US/08/973,965
EARLIER FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: AT A 1007/95
EARLIER FILING DATE: 1995-06-13
EARLIER APPLICATION NUMBER: PCT/AT96/00106
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 95
TYPE: DNA
ORGANISM: synthetic construct
US-08-973-965-39

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 95;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgagc 20
DB 23 GAGCTGACTGGTTGAGGC 4

RESULT 4
US-09-098-287A-5/c
Sequence 5, Application US/09098287A
Patent No. 615890
GENERAL INFORMATION:
APPLICANT: BOTTIN
APPLICANT: Steinhilber, Carl M.
APPLICANT: Sodell, Ulf, HE
TITLE OF INVENTION: A method for in vitro molecular
FILE REFERENCE: evolution of protein function
CURRENT APPLICATION NUMBER: US/09/098,287
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: GB9712512.4
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 710
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Theoretical insert
US-09-098-287A-5

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 710;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggttgagc 20
DB 461 GAGCTGACTGGTTGAGGC 442

RESULT 5
US-08-613-965-1/c
Sequence 1, Application US/08613965
Patent No. 5916745
GENERAL INFORMATION:
APPLICANT: Robert M. Cook and Ahmed Raafat
TITLE OF INVENTION: Method for Determination
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB
MEDIUM TYPE: Storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,965
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-290
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5916745E
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1130
TYPE: nucleotides
STRANDEDNESS: Single
MOLECULE TYPE: Linear
DESCRIPTION: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bovine
STRAIN:
INDIVIDUAL ISOLATE: ATCS
CELL TYPE: mammary gland
FEATURE:
NAME/KEY: CDNA in pATCS
LOCATION: mammary gland CDNA and
IDENTIFICATION METHOD: encoded peptide
OTHER INFORMATION: Sequencing
of acetyl coenzyme A

OTHER INFORMATION: synthetase
US-08-613-965-1

Query Match 100.0%; Score 20; DB 2; Length 1130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggtgaagc 20
|||||
DB 836 GAGCTGACTGGGTGAAGC 817

RESULT 6

US-08-918-966-1/c
; Sequence 1, Application US/08918966
; Patent No. 5981187
; GENERAL INFORMATION:
; APPLICANT: Robert M. Cook and Ahmed Raafat
; TITLE OF INVENTION: Method For Determination
; TITLE OF INVENTION: of Bovine Milk Production Potential
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,966
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: NO. 5981187e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1130
; TYPE: nucleotides
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bovine
; STRAIN:
; INDIVIDUAL ISOLATE: ATC5
; CELL TYPE: mammary gland
; FEATURE:
; NAME/KEY: cDNA in PATC5
; LOCATION: mammary gland cDNA and
; LOCATION: encoded peptide
; IDENTIFICATION METHOD: Sequencing
; OTHER INFORMATION: Encodes a portion
; OTHER INFORMATION: of acetyl coenzyme A
; OTHER INFORMATION: synthetase

US-08-918-966-1

Query Match 100.0%; Score 20; DB 2; Length 1130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggtgaagc 20
|||||
DB 836 GAGCTGACTGGGTGAAGC 817

RESULT 7

US-08-921-655-1/c
; Sequence 1, Application US/08921655
; Patent No. 6013496
; GENERAL INFORMATION:
; APPLICANT: Robert M. Cook and Ahmed Raafat
; TITLE OF INVENTION: Method For Determination
; TITLE OF INVENTION: of Bovine Milk Production Potential
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: NO. 6013496e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1130
; TYPE: nucleotides
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bovine
; STRAIN:
; INDIVIDUAL ISOLATE: ATC5
; CELL TYPE: mammary gland
; FEATURE:
; NAME/KEY: cDNA in PATC5
; LOCATION: mammary gland cDNA and
; LOCATION: encoded peptide
; IDENTIFICATION METHOD: Sequencing
; OTHER INFORMATION: Encodes a portion
; OTHER INFORMATION: of acetyl coenzyme A
; OTHER INFORMATION: synthetase
US-08-921-655-1

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Query Match 100.0%; Score 20; DB 3; Length 1130;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
Db 836 GAGCTGACTGCTTGAAGC 817

RESULT 8
US-08-218-303-15/c
Sequence 15, Application US/08218303
Patent No. 5547867
GENERAL INFORMATION:
APPLICANT: Kara, Bhupendra V.
APPLICANT: Hockney, Robert C.
TITLE OF INVENTION: FERMENTATION PROCESS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,303
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841,533
FILING DATE: 26-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 143..943
US-08-218-303-15

Query Match 100.0%; Score 20; DB 1; Length 1140;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
Db 1076 GAGCTGACTGCTTGAAGC 1057

RESULT 9
US-08-338-793D-60/c
Sequence 60, Application US/08338793D

Patent No. 5840521
GENERAL INFORMATION:
APPLICANT: Barth, Peter Thomas
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY CUSHMAN
ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF
STREET: 100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.44 MB storage
COMPUTER: IBM PC/XT/AT Compatibles
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word or ASCII editors
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,793D
FILING DATE: 08 Nov. 5840521-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842,081
FILING DATE: 26-Feb-92
CLASSIFICATION: 435
APPLICATION NUMBER: 9104017.0
FILING DATE: 26-Feb-91
APPLICATION NUMBER: 9109188.4
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-338-793D-60

Query Match 100.0%; Score 20; DB 2; Length 1140;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
Db 1076 GAGCTGACTGCTTGAAGC 1057

RESULT 10
US-08-447-430A-42
Sequence 42, Application US/08447430A
Patent No. 5916558
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Recombinant polypeptides and peptides,
TITLE OF INVENTION: nucleic acids coding for the same and use of these
NUMBER OF INVENTION: polypeptides and peptides in the diagnostic of
NUMBER OF SEQUENCES: 43
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: plasmid vector
; HYPOTHETICAL: NO
US-08-447-430A-42

Query Match          100.0%; Score 20; DB 2; Length 3301;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
   |||
Db 2612 GAGCTGACTGGGTTGAAGC 2631

RESULT 11
US-08-447-430A-40
; Sequence 40, Application US/08447430A
; Patent No. 5916558
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant polypeptides and peptides,
; TITLE OF INVENTION: nucleic acids coding for the same and use of these
; TITLE OF INVENTION: polypeptides and peptides in the diagnostic of
; NUMBER OF SEQUENCES: 43
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: plasmid vector
; HYPOTHETICAL: NO
US-08-447-430A-40

Query Match          100.0%; Score 20; DB 2; Length 3423;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
   |||
Db 2730 GAGCTGACTGGGTTGAAGC 2749

RESULT 12
US-08-447-430A-41
; Sequence 41, Application US/08447430A
; Patent No. 5916558
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant polypeptides and peptides,
; TITLE OF INVENTION: nucleic acids coding for the same and use of these
; TITLE OF INVENTION: polypeptides and peptides in the diagnostic of
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; TITLE OF INVENTION: tuberculosis.
; NUMBER OF SEQUENCES: 43
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: plasmid vector
; HYPOTHETICAL: NO
US-08-447-430A-41

Query Match          100.0%; Score 20; DB 2; Length 3474;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
   |||
Db 2783 GAGCTGACTGGGTTGAAGC 2802

RESULT 13
US-08-318-837-10
; Sequence 10, Application US/08318837
; Patent No. 5981277
; GENERAL INFORMATION:
; APPLICANT: FRANSSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
; APPLICANT: ANDRE; VAN HEUVERSWEY, HUGO
; TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
; TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAP
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,837
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP 93/01022
; FILING DATE: 28-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 92.401.231.3
; FILING DATE: 30-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
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us-09-631-709-2.rni

LENGTH: 3474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pMTNF-MPH
US-08-318-837-10

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 3474;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
DB 2783 GAGCTGACTGCTTGAAGC 2802

RESULT 14
US-08-500-860A-2
Sequence 2, Application US/08500860A
Patent No. 5891678
GENERAL INFORMATION:
APPLICANT: LUCAS, RUDOLPH
APPLICANT: DE BERTSELIER, PATRICK
APPLICANT: PRANSEN, LUCIE
TITLE OF INVENTION: TNF-MUTEINS, A PROCESS FOR PREPARING THEM AND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,860A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
TELECOMMUNICATION INFORMATION: 1487-8
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4009 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: circular
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pig2
US-08-500-860A-2

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 4009;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
DB 2185 GAGCTGACTGCTTGAAGC 2166

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
DB 3320 GAGCTGACTGCTTGAAGC 3339

RESULT 15
US-08-929-967-4/C
Sequence 4, Application US/08929967
Patent No. 5891637
GENERAL INFORMATION:
APPLICANT: Ruppert, Siegfried J.W.
TITLE OF INVENTION: Construction of Full-Length cDNA Libraries
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Alupalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,967
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
TELECOMMUNICATION INFORMATION: P1035R1
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4245 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-929-967-4

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 4245;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagctgactggttgaagc 20
DB 2185 GAGCTGACTGCTTGAAGC 2166

Search completed: December 13, 2001, 13:29:59
Job time: 193 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:43:08 ; Search time 496.49 Seconds
(without alignments)
34.535 Million cell updates/sec

Title: US-09-631-709-2

Perfect score: 20
Sequence: 1 gagctgactggttgaaagc 20.

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*

1:	/SID2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2:	/SID2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3:	/SID2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4:	/SID2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5:	/SID2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6:	/SID2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7:	/SID2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8:	/SID2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9:	/SID2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10:	/SID2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11:	/SID2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12:	/SID2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13:	/SID2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14:	/SID2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15:	/SID2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16:	/SID2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17:	/SID2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18:	/SID2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19:	/SID2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20:	/SID2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21:	/SID2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22:	/SID2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	22	AAH46615
2	20	100.0	20	22	AAF62503
3	20	100.0	41	17	AAT36954
4	20	100.0	41	17	AAT36970
5	20	100.0	41	17	AAT36971
6	20	100.0	91	17	AAT36956
7	20	100.0	91	17	AAT36974
8	20	100.0	169	18	AAV77033
9	20	100.0	600	7	AAH60881
10	20	100.0	600	7	AAH60882
11	20	100.0	710	20	AAH00997

C	12	20	100.0	1097	21	AAZ34980
C	13	20	100.0	1130	20	AAZ35503
C	14	20	100.0	1130	21	AAZ87413
C	15	20	100.0	1140	13	AAO27876
C	16	20	100.0	1140	14	AAO36947
C	17	20	100.0	1632	11	AAO03698
C	18	20	100.0	3000	7	AAH60892
C	19	20	100.0	3000	8	AAH60882
C	20	20	100.0	3327	22	AAH60859
C	21	20	100.0	3369	22	AAH62653
C	22	20	100.0	3423	12	AAH66255
C	23	20	100.0	3423	12	AAO11083
C	24	20	100.0	3474	20	AAH08615
C	25	20	100.0	3474	13	AAO29146
C	26	20	100.0	3880	22	AAO51546
C	27	20	100.0	3954	22	AAE25570
C	28	20	100.0	3976	22	AAH66260
C	29	20	100.0	3985	22	AAH66256
C	30	20	100.0	4009	15	AAO81201
C	31	20	100.0	4163	15	AAO70219
C	32	20	100.0	4196	21	AAO29134
C	33	20	100.0	4207	21	AAA30825
C	34	20	100.0	4222	10	AAH92031
C	35	20	100.0	4269	21	AAH92038
C	36	20	100.0	4300	21	AAA92002
C	37	20	100.0	4369	21	AAH29135
C	38	20	100.0	4464	21	AAZ9578
C	39	20	100.0	4466	22	AAH6264
C	40	20	100.0	4466	10	AAH90286
C	41	20	100.0	4466	15	AAO58637
C	42	20	100.0	4586	19	AAV43441
C	43	20	100.0	4608	10	AAH90288
C	44	20	100.0	4643	13	AAO25112
C	45	20	100.0	4651	10	AAH92044

ALIGNMENTS

RESULT 1

ID	AAH46615	standard; DNA; 20 BP.
AC	AAH46615:	
DT	17-SEP-2001	(first entry)
DE	Synthetic oligonucleotide #18.	
KW	Helicobacter pylori; alpha-1,2-fucosyltransferase;	
KW	fucose-containing sugar production; Lewis antigen; ss.	
OS	Synthetic.	
PN	MO200146400-A1.	
XX	28-JUN-2001.	
XX	20-DEC-2000; 2000MO-JP09033.	
XX	21-DEC-1999; 99JP-0362243.	
PA	(KYOW) KYOWA HAKKO KOGYO KK.	
PI	Endo T, Koizumi S, Tabata K, Ozaki A;	
DR	WPI; 2001-418061/44.	
PT	Modified alpha-1,2-fucosyltransferase gene and its expression product	
PT	for efficient production of fucose-containing sugars such as Lewis	
PS	antigen	
PS	Example 2; Page 62; 69pp; Japanese.	

Mouse F1271 expres
Clone ATC 5 polyu
Bovine acetyl coen
Ricin A gene from
Partial sequence o
Recombinant plasm
Sequence of plasm
Sequence contg. ce
Plasmid GHRH1-29YA
pGHRH-4 44SK const
Plasmid pIGR1 for
pIGR12 expression
pMNF-MPH plasmid
Expression plasmid
Vector pSRM4 DNA.
Plasmid GHRH1-29YW
pGHRH1-44WTSK685 c
Plasmid pLPRS. S
Plasmid pIG2 for T
pNF-kappaB-d2EGFP
Expression casset
Sequence of recomb
Sequence of recomb
pCBE5-d2EGFP report
pCBE5-d2EGFP const
Partial sequence o
Plasmid GHRH1-29YA
pPR104-4 sequence.
DNA sequence of th
Plasmid pPR70-1.
DHFR-AP fusion pr
Recombinant plasm
Sequence of recomb

CC The invention relates to DNA encoding a modified form of the
 CC alpha-1,2-fucosyltransferase of Helicobacter pylori. The
 CC polypeptide sequence of the AAAAAAG sequence and/or the
 CC repeats has been modified in the DNA sequence and/or the number of TAA
 CC useful in the production of large amounts of fucose-containing
 CC sugars, such as Lewis x and Lewis y antigens for medicinal use. The present
 CC sequence is an oligonucleotide provided in the specification.
 SO Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 20; DB 22; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaaagc 20
 Db 1 gagctgactgggttgaaagc 20

RESULT 2
 ID AAF62503 standard; DNA; 20 BP.
 AC AAF62503;

DT 08-MAY-2001 (first entry)
 DE Primer for glk gene.
 KW Guanosine 5'-diphosphofucose; GDP-fucose;
 KW Guanosine 5'-diphospho-4-keto-6-deoxymannose; GKDW; immunotherapy;
 KW cardiovascular; infection; ss.
 OS Synthetic.
 PN EPI076096-A1.
 PD 14-FEB-2001.
 PF 10-AUG-2000; 2000EP-0117167.
 PR 10-AUG-1999; 99JP-0225889.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PI Koizumi S, Nagano H, Endo T, Tabata K, Ozaki A;
 DR WPI; 2001-193203/20.
 XX Producing guanosine 5'-diphosphofucose (GDP-fucose) useful as a
 XX substrate of complex carbohydrates for immunotherapy comprises
 XX employing microorganisms that convert guanosine
 XX 5-diphospho-4-keto-6-deoxymannose to GDP-fucose -
 PS Example 1; Page 11; 19pp; English.

CC The present invention relates to producing guanosine
 CC 5'-diphosphofucose (GDP-fucose) by employing an enzyme source
 CC that is a culture broth of microorganisms. GDP-fucose is useful
 CC as a synthetic substrate of complex carbohydrates that are useful
 CC diseases, or infections by bacteria or viruses. Cardiovascular
 CC 5'-diphospho-4-keto-6-deoxymannose (GKDW) is useful as
 CC an intermediate for the production of GDP-fucose.
 SO Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 20; DB 22; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaaagc 20
 Db 1 gagctgactgggttgaaagc 20

RESULT 3
 ID AAT36954 standard; DNA; 41 BP.
 AC AAT36954;

DT 16-FEB-1997 (first entry)
 DE Primer used in transcription free amplification method.
 KW Amplification; primer; template; transcription; diagnosis;
 KW medicine; environmental analysis; forensic analysis; ss.
 OS Synthetic.
 PN AT9501007-A.
 PD 15-JUL-1996.
 PF 13-JUN-1995; 95AT-0001007.
 PR 13-JUN-1995; 95AT-0001007.
 PA (HIMM) HIMMELER G.
 DR WPI; 1996-322132/33.
 XX Transcription free amplification of nucleic acid - with
 XX amplification and strand sepn. of prod. at same temp., useful for in
 XX vitro clinical diagnosis

PS Example 1; Page 9; 25pp; German.
 CC Transcription free amplification of a nucleic acid sequence (A) with
 CC enzymes, comprises: (1) optionally, before amplification, converting
 CC (A) at least partly to individual strands by separation and/or
 CC transcription; (2) adding nucleotides (1) having a sequence
 CC essentially complementary to the ends of (A) having a sequence
 CC as starting points complementary to the ends of (A) and being able to act
 CC incorporated into the amplification product; (3) amplification,
 CC optionally with addition of other required chemical building
 CC blocks; and (4) at least partial separation of the amplification
 CC product into its individual strands. The method is useful for in
 CC vitro diagnosis in human or veterinary medicine or for environmental
 CC (eliminates the need for temperature cycling). Two primers
 CC (AAT36954, AAT36955) were used to amplify a template molecule (AAT36956)
 SO using the method.

Query Match
 Best Local Similarity 100.0%; Score 20; DB 17; Length 41;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactgggttgaaagc 20
 Db 22 gagctgactgggttgaaagc 3

RESULT 4
 ID AAT36970 standard; DNA; 41 BP.
 AC AAT36970;


```
DT 17-FEB-1997 (first entry)
XX
XX Oligonucleotide used in transcription free amplification method.
DE
XX Amplification; primer; template; transcription; diagnosis;
KW medicine; environmental analysis; forensic analysis; ss.
XX
XX Synthetic.
OS
XX AT9501007-A.
PN
XX 15-JUL-1996.
PD
XX
XX 13-JUN-1995; 95AT-0001007.
PF
XX
XX 13-JUN-1995; 95AT-0001007.
PR
XX
XX (HIMM/) HIMMLER G.
PA
XX
XX WPI; 1996-322132/33.
DR
XX
XX Transcription free amplification of nucleic acid - with
PT amplification and strand sepn. of prod. at same temp., useful for in
PT vitro clinical diagnosis
PS
XX Example 8; Page 20; 25pp; German.
PS
XX Transcription free amplification of a nucleic acid sequence (A) with
CC enzymes; comprises: (1) optionally, before amplification, converting
CC (A) at least partly to individual strands by separation and/or
CC transcription; (2) adding nucleotides (I) having a sequence
CC essentially complementary to the ends of (A) and being able to act
CC as starting points for nucleic acid synthesis and becoming
CC incorporated into the amplification product; (3) amplification,
CC optionally with addition of other required chemical building
CC blocks; and (4) at least partial separation of the amplification
CC product into its individual strands. The method is useful for in
CC vitro diagnosis in human or veterinary medicine, or for environmental
CC or forensic analysis. The process is simple and inexpensive
CC (eliminates the need for temperature cycling). Four
CC oligonucleotides (AAT36970-73) were used to amplify a template molecule
CC (AAT36974), and generate a double stranded product using the method.
CC
XX
XX Sequence 41 BP; 7 A; 14 C; 15 G; 5 T; 0 other;
SQ
XX
XX
XX Query Match 100.0%; Score 20; DB 17; Length 41:
XX Best Local Similarity 100.0%; Pred. No. 0.73;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactggttgaagc 20
DB 20 gagctgactggttgaagc 39
|||||
RESULT 5
AAT36971/C
ID AAT36971 standard; DNA; 41 BP.
XX
XX AAT36971;
AC
XX
XX 17-FEB-1997 (first entry)
DT
XX
XX Oligonucleotide used in transcription free amplification method.
DE
XX Amplification; primer; template; transcription; diagnosis;
KW medicine; environmental analysis; forensic analysis; ss.
XX
XX Synthetic.
OS
XX AT9501007-A.
PN
XX
XX 15-JUL-1996.
PD
XX
```

```
XX
XX 13-JUN-1995; 95AT-0001007.
PF
XX
XX 13-JUN-1995; 95AT-0001007.
PR
XX
XX (HIMM/) HIMMLER G.
PA
XX
XX WPI; 1996-322132/33.
DR
XX
XX Transcription free amplification of nucleic acid - with
PT amplification and strand sepn. of prod. at same temp., useful for in
PT vitro clinical diagnosis
PS
XX Example 8; Page 20; 25pp; German.
PS
XX Transcription free amplification of a nucleic acid sequence (A) with
CC enzymes; comprises: (1) optionally, before amplification, converting
CC (A) at least partly to individual strands by separation and/or
CC transcription; (2) adding nucleotides (I) having a sequence
CC essentially complementary to the ends of (A) and being able to act
CC as starting points for nucleic acid synthesis and becoming
CC incorporated into the amplification product; (3) amplification,
CC optionally with addition of other required chemical building
CC blocks; and (4) at least partial separation of the amplification
CC product into its individual strands. The method is useful for in
CC vitro diagnosis in human or veterinary medicine, or for environmental
CC or forensic analysis. The process is simple and inexpensive
CC (eliminates the need for temperature cycling). Four
CC oligonucleotides (AAT36970-73) were used to amplify a template molecule
CC (AAT36974), and generate a double stranded product using the method.
CC
XX
XX Sequence 41 BP; 5 A; 15 C; 14 G; 7 T; 0 other;
SQ
XX
XX
XX Query Match 100.0%; Score 20; DB 17; Length 41:
XX Best Local Similarity 100.0%; Pred. No. 0.73;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gagctgactggttgaagc 20
DB 22 GACCTGACTGCTTGGAAGC 3
|||||
RESULT 6
AAT36956/C
ID AAT36956 standard; DNA; 91 BP.
XX
XX AAT36956;
AC
XX
XX 17-FEB-1997 (first entry)
DT
XX
XX Template used in transcription free amplification method.
DE
XX Amplification; primer; template; transcription; diagnosis;
KW medicine; environmental analysis; forensic analysis; ss.
XX
XX Synthetic.
OS
XX AT9501007-A.
PN
XX
XX 15-JUL-1996.
PD
XX
XX 13-JUN-1995; 95AT-0001007.
PF
XX
XX 13-JUN-1995; 95AT-0001007.
PR
XX
XX (HIMM/) HIMMLER G.
PA
XX
XX WPI; 1996-322132/33.
DR
XX
XX Transcription free amplification of nucleic acid - with
PT amplification and strand sepn. of prod. at same temp., useful for in
PT vitro clinical diagnosis
```

XX Example 1; Page 9; 25pp; German.
 PS Transcription free amplification of a nucleic acid sequence (A) with
 CC enzymes, comprises: (1) optionally, before amplification, converting
 CC (A) at least partly to individual strands by separation and/or
 CC transcription; (2) adding nucleotides (1) having a sequence
 CC essentially complementary to the ends of (A) and being able to act
 CC as starting points for nucleic acid synthesis and becoming
 CC incorporated into the amplification product; (3) amplification,
 CC optionally with addition of other required chemical building
 CC blocks; and (4) at least partial separation of the amplification
 CC product into its individual strands. The method is useful for in
 CC vitro diagnosis in human or veterinary medicine, or for environmental
 CC or forensic analysis. The process is simple and inexpensive
 CC (AA736954, AA736955) were used to amplify a template molecule
 CC using the method.
 XX Sequence 91 BP; 13 A; 29 C; 31 G; 18 T; 0 other;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 20; DB 17; Length 91;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 gagctgactgggtgaagc 20
 DB 22 GAGCTGACTGGGTGAAGC 3

RESULT 7
 ID AA736974/c
 XX AA736974 standard; DNA; 91 BP.
 AC AA736974;
 XX
 DT 17-FEB-1997 (first entry)
 DE Template used in transcription free amplification method.
 XX
 KW Amplification: primer; template; transcription; diagnosis;
 KW medicine; environmental analysis; forensic analysis; ss.
 OS Synthetic.
 XX
 PN AT9501007-A.
 PD 15-JUL-1996.
 XX
 PF 13-JUN-1995; 95AT-0001007.
 XX
 PR 13-JUN-1995; 95AT-0001007.
 XX
 PA (HIMM) HIMMELER G.
 XX
 DR WPI; 1996-322132/33.
 XX
 PR Transcription free amplification of nucleic acid - with
 XX amplification and strand sepn. of prod. at same temp., useful for in
 XX vitro clinical diagnosis
 XX
 PS Example 8; Page 20; 25pp; German.
 CC Transcription free amplification of a nucleic acid sequence (A) with
 CC enzymes, comprises: (1) optionally, before amplification, converting
 CC (A) at least partly to individual strands by separation and/or
 CC transcription; (2) adding nucleotides (1) having a sequence
 CC essentially complementary to the ends of (A) and being able to act
 CC as starting points for nucleic acid synthesis and becoming
 CC incorporated into the amplification product; (3) amplification,
 CC optionally with addition of other required chemical building
 CC blocks; and (4) at least partial separation of the amplification
 CC product into its individual strands. The method is useful for in
 CC vitro diagnosis in human or veterinary medicine, or for environmental
 CC or forensic analysis. The process is simple and inexpensive
 CC (AA736954, AA736955) were used to amplify a template molecule
 CC using the method.
 XX Sequence 91 BP; 13 A; 29 C; 31 G; 18 T; 0 other;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 20; DB 17; Length 91;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 gagctgactgggtgaagc 20
 DB 22 GAGCTGACTGGGTGAAGC 3

RESULT 8
 ID AA77033
 XX AA77033 standard; DNA; 169 BP.
 AC AA77033;
 XX
 DT 16-MAR-1999 (first entry)
 DE Staphylococcus aureus contig SEQ ID #2722.
 XX
 KW Computer readable medium; vaccine; S. aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 XX toxic shock syndrome; de.
 OS Staphylococcus aureus.
 XX
 PN EP76519-A2.
 PD 30-JUL-1997.
 XX
 PF 07-JAN-1997; 97EP-0100117.
 XX
 PR 05-JAN-1996; 96US-0009861.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Barash SC, Choi GH, Dillon PT, Fannon MR, Kunsch CA;
 PI Rosen CA;
 XX
 XX WPI; 1997-374922/35.
 XX
 PR Polynucleotide(s) and proteins derived from Staphylococcus aureus
 XX stored on computer readable medium and used in the production of
 XX anti-S. aureus vaccines
 XX
 PS Claim 1; Page 2318; 3271pp; English.
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random readable
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S. aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S. aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S. aureus in a sample. S. aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating

CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.
XX
SQ Sequence 169 BP; 39 A; 51 C; 47 G; 31 T; 1 other;

Query Match 100.0%; Score 20; DB 18; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactgggttgaagc 20
|||||
DB 112 gagctgactgggttgaagc 131

RESULT 9

AA060881/C
ID AA060881 standard; DNA; 600 BP.

XX
AC AA060881;

XX 22-OCT-1991 (first entry)

DE Sequence encoding novel polypeptide with interferon activity.

XX IFN: antitumour; antiviral; pGI-101; pGSII-102.

XX Key Location/Qualifiers

XX CDS 115..558

XX FT /*tag= a

XX JP61033200-A.

XX 17-FEB-1986.

XX 22-MAY-1985; 85JP-0108299.

XX 22-MAY-1984; 84US-0613067.

XX (ASAHI) ASAHI CHEMICAL IND KK.

XX WPI: 1986-240788/37.

XX P-PSDB; AAP61073.

XX Polypeptide(s) with human immune interferon activities - obt'd. by

XX culturing transformed microbe e.g. E.coli transformed with

XX pGSII-102 (J6 17/2/86).

XX Disclosure: Page 1126; 16pp; Japanese.

XX The gene product has human immune interferon activity, excellent in

XX antitumour and antiviral treatment. The product may be expressed

XX from a suitable host eg. E.coli, transformed with plasmids pGI-101

XX or pGS-102.

XX Sequence 600 BP; 212 A; 108 C; 122 G; 158 T; 0 other;

RESULT 10

AA060882/C
ID AA060882 standard; DNA; 600 BP.

XX
AC AA060882;

XX

DT 22-OCT-1991 (first entry)

XX Sequence encoding novel polypeptide with interferon activity.

XX IFN: antitumour; antiviral; pGI-101; pGSII-102.

XX Key Location/Qualifiers

XX CDS 115..558

XX FT /*tag= a

XX JP61033200-A.

XX 17-FEB-1986.

XX 22-MAY-1985; 85JP-0108299.

XX 22-MAY-1984; 84US-0613067.

XX (ASAHI) ASAHI CHEMICAL IND KK.

XX WPI: 1986-240788/37.

XX P-PSDB; AAP61074.

XX Polypeptide(s) with human immune interferon activities - obt'd. by

XX culturing transformed microbe e.g. E.coli transformed with

XX pGSII-102 (J6 17/2/86).

XX Disclosure: Page 1127; 16pp; Japanese.

XX The gene product has human immune interferon activity, excellent in

XX antitumour and antiviral treatment. The product may be expressed

XX from a suitable host eg. E.coli, transformed with plasmids pGI-101

XX or pGS-102.

XX Sequence 600 BP; 213 A; 108 C; 121 G; 158 T; 0 other;

RESULT 11

AA00097/C
ID AA00097 standard; DNA; 710 BP.

XX
AC AA00097;

XX 12-MAY-1999 (first entry)

XX Mutated tetracycline resistance gene fragment of pBR322 clone FIND1.

XX PCR: primer; fragment; segment; insert; clone; cloning; FIND;

XX fragment inducible nucleotide diversity; DNA shuffling; antibody;

XX modify; tetracycline; revertant; ss.

XX Synthetic.

XX W09858080-A1.

XX 23-DEC-1998.

XX 16-JUN-1998; 98WO-GB01757.

XX 16-JUN-1997; 97GB-0012512.

XX (BIOI-) BIOINVENT INT AB.

XX (CRIP/) CRIPPS J E.

XX

FT /product- ACS
 FT /note= "Acetyl coenzyme A synthetase, this sequence
 FT contains 2 in frame stop codons"
 FT /transl_except- (pos:46..48, aa:Xaa)
 FT /transl_except- (pos:130..132, aa:Xaa)
 FT /transl_except- (pos:349..351, aa:Xaa)
 FT /transl_except- (pos:472..474, aa:Xaa)
 FT /transl_except- (pos:525..527, aa:Xaa)
 FT /transl_except- (pos:784..786, aa:Xaa)
 FT /transl_except- (pos:805..807, aa:Xaa)
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 FT /transl_except- (pos:868..870, aa:Xaa)
 FT /note= "Xaa = unknown"
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 PN US5981187-A.
 PD 09-NOV-1999.
 XX
 XX 26-AUG-1997; 970S-0918966.
 XX
 XX 08-MAR-1996; 96US-0613965.
 XX
 PA (UNMS) UNIV MICHIGAN STATE.
 XX
 PI Raafat AM, Cook RM;
 XX
 XX WPI: 1999-633309/54.
 DR P-PSDB; AAY52098.
 XX
 PT Determining potential milk production in calves -
 PS Example 1; Fig 26A; 41pp: English.
 XX
 CC This is the clone ATC 5 nucleotide sequence isolated using AR8 CDNA
 CC (AA235301-235302: partial ACS sequences) from bovine mammary gland
 CC tissue. The sequence is thought to encode bovine acetyl coenzyme A
 CC synthetase (ACS). AR8 sequences were isolated via screening with rabbit
 CC anti-ACS sera. ACS is involved in the synthesis of acetyl coenzyme A
 CC which is a major substrate for milk synthesis and occupies a central
 CC position in the metabolism of Holstein mammary gland tissue. ACS activity
 CC is directly related to milk production. The AR8 sequences are used in a
 CC method for determining the potential milk production potential in calves
 CC before milk production and breeding begins. The method involves
 CC determining the level of ACS or mRNA encoding ACS in the mammary tissue
 CC of a calf. The method allows an estimation of the milk production potential of
 CC a calf. The method can be used in selection and/or breeding programmes to
 CC enhance milk production and to identify cows which may be in need of
 CC treatment to augment lactation.
 CC
 CC Sequence 1130 BP; 198 A; 351 C; 305 G; 268 T; 8 other;
 SQ
 OY 1 gagactgactgggttgaagc 20
 DB 836 GAGCTGACTGGGTGAAGC 817
 ID AA287413/C
 ID AA287413 standard; cDNA: 1130 BP.
 AC AA287413;
 XX
 XX 22-MAY-2000 (first entry)
 DE Bovine acetyl coenzyme A synthetase (ACS) cDNA clone ATC5.
 XX
 XX Acetyl coenzyme A synthetase; ACS; bovine; acetyl CoA; lactation;
 KW fusion protein; beta-galactosidase; antibody; affinity purification;

KW breeding programme; milk production; selection; clone ATC5; ss.
 XX
 OS Bos taurus var. Holstein.
 XX
 FH Key Location/Qualifiers
 FT CDS 220..1130
 FT /tag= a
 FT /partial
 FT /product= "Bovine acetyl coenzyme A synthetase (ACS)"
 FT /note= "No stop codon given in the specification"
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 FT /transl_except- (pos:523..525, aa:Xaa)
 FT /transl_except- (pos:784..786, aa:Xaa)
 FT /transl_except- (pos:805..807, aa:Xaa)
 FT /transl_except- (pos:847..849, aa:Xaa)
 FT /transl_except- (pos:868..870, aa:Xaa)
 FT /note= "Xaa is unknown"
 FT
 PN US6013496-A.
 PD 11-JAN-2000.
 XX
 XX 26-AUG-1997; 970S-0921655.
 XX
 XX 08-MAR-1996; 96US-0613965.
 XX
 PA (UNMS) UNIV MICHIGAN STATE.
 XX
 PI Cook RM, Raafat AM;
 XX
 XX WPI: 2000-170260/15.
 DR P-PSDB; AAY77268.
 XX
 PT New isolated acetyl coenzyme A synthetase (ACS) fusion proteins, for
 PT affinity purification of anti-ACS antibodies which are used to identify
 PT cows with high milk production potential -
 PS Claim 1; Fig 26A; 50pp: English.
 XX
 CC The invention relates to fusion proteins comprising bovine acetyl
 CC coenzyme A synthetase (ACS), and to nucleotide sequences encoding
 CC the proteins. ACS catalyses the acetate activation reaction, which
 CC generates acetyl CoA. Acetyl CoA is a major substrate for milk
 CC synthesis, and ACS activity is directly correlated with milk
 CC production. The fusion protein of the invention is either a beta-
 CC galactosidase/ACS fusion protein in which the ACS component is encoded
 CC by DNA (AA287413) present in plasmid pUC19-pATC5 (ATCC 98008) or a
 CC fusion protein in which the ACS component is encoded by DNA
 CC (AA287415-287416) present in plasmid pUC19-pAR8 (ATCC 209191). cDNA was
 CC produced via reverse transcription from poly(A)+ RNA isolated from bovine
 CC mammary tissue taken at peak lactation. The cDNAs were cloned into the
 CC EcoRI site of lambda phage g11, producing beta-galactosidase/cDNA
 CC fusion genes, and the phage library screened with polyclonal rabbit
 CC anti-bovine ACS antibodies produced against purified bovine (Holstein)
 CC ACS. A positive plaque, lambda AR8, was identified and the cDNA insert
 CC (cloned into pUC19) sequenced. Lambda AR8 was also used to infect
 CC Escherichia coli, in order to produce beta-galactosidase/ACS fusion
 CC protein for assay of ACS activity. An AR8 probe was used to rescreen the
 CC bovine mammary gland cDNA phage library, and another positive plaque
 CC identified (lambda ATC5). The ATC5 insert was cloned into pUC19 and
 CC sequenced, and the ACS fusion protein activity assayed. The fusion
 CC proteins of the invention may be used for affinity purification of rabbit
 CC anti-ACS antibodies. The antibodies are used to determine levels of ACS
 CC in bovine mammary tissue, particularly to identify cows with potential
 CC for high level milk production in breeding programmes. Anti-ACS
 CC antibodies, affinity purified with ACS fusion protein, allow calves with
 CC high levels of ACS (indicating potential for high level milk production,
 CC and therefore preferred for breeding) to be identified. This means that
 CC relatively fewer animals need to be bred, and selection of animals for
 CC high level ACS production will result in significant increases in milk
 CC production. The present sequence represents the bovine ACS cDNA
 CC clone ATC5.

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Page 8

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XX      SQ      Sequence 1130 BP; 198 A; 351 C; 305 G; 268 T; 8 other;
Query Match
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      836 GAGCTGACTGCGTTGAAGC 817
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ID      AAQ27876 standard; DNA; 1140 BP.
AC      AAQ27876;
DT      08-FEB-1993 (first entry)
DE      Ricin A gene from PIC1102.
KW      pH; temperature; cultivation; host; soluble; ss.
OS      Synthetic.
FX      Key
FH      Location/Qualifiers
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FT      /note= "region indicated in the specification as
FT      90..92 comprising a TTP promoter, S-D and IDS"
FT      /tag= b
FT      /label= translation_initiation_codon
FT      /note= "first translation initiation codon out of
FT      139..131 frame with that of Ricin A coding region"
FT      /tag= c
FT      /label= stop_codon
FT      /note= "in-frame termination codon prior to the
FT      132..135 ricin A initiation codon"
FT      /tag= d
FT      /note= "SD capable of re-initiating translation
FT      143..946
FT      /tag= e
FT      /label= ricin_A
FT      947..1140
FT      /tag= f
FT      /note= "region comprising terminator"
XX      EPS01692-A.
XX      PD      02-SEP-1992.
XX      XX
XX      PF      21-FEB-1992; 92EP-0301466.
XX      PR      26-FEB-1991; 91GB-0003925.
XX      PR      26-FEB-1991; 91GB-0003925.
XX      XX      26-FEB-1991; 91GB-0004016.
XX      PA      (ICIL ) IMPERIAL CHEM IND PLC.
XX      PI      Filtron JE, Hockney RC, Kara BV;
XX      DR      WPI: 1992-294124/36.
XX      PT      P-PSDB; AAR30722.
XX      PT      Prepn. of soluble recombinant polypeptide(s), esp. ricin A - by
XX      PT      adjusting pH and/or temp. during cultivation to increase yield of
XX      PT      soluble prod.

```

```

XX      SQ      Sequence 1140 BP; 319 A; 256 C; 248 G; 317 T; 0 other;
Query Match
Best Local Similarity 100.0%; Score 20; DB 13; Length 1140;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 gagctgactgggttgaagc 20
DB      1076 GAGCTGACTGCGTTGAAGC 1057
Prepn. of ricin A comprises cultivating a host, including a DNA
sequence which encodes ricin A, e.g. from PIC1102, in a nutrient
medium for an initial period at a first pH value which favours growth
of the host; and cultivation the host for a further period at a pH
lower than the first pH value, and optionally further period at a pH
the terminal portion of the cultivation and harvesting the host during the
cultivation of hosts, high yields of soluble recombinant ricin A
are obtained.

```

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Job time: 8183 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2001, 15:34:38 ; Search time 1854.2 Seconds
(without alignments)
177.944 Million cell updates/sec

Title: US-09-631-709-2

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Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
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28: em_un:*
29: em_vl:*
30: em_htgo_hum:*
31: em_htgo_inv:*
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33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rnd:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	41	6	A58755	A58755 Sequence 1
3	20	100.0	91	6	A58757	A58757 Sequence 3
4	20	100.0	91	6	A58758	A58758 Sequence 4
5	20	100.0	162	1	NGSIPUB	X60747 N.gonorrhoe
6	20	100.0	600	6	E00695	E00695 A plasmid p
7	20	100.0	710	6	A81874	A81874 Sequence 5
8	20	100.0	710	6	AR120677	AR120677 Sequence 5
9	20	100.0	100073	6	100073	100073 Sequence 2
10	20	100.0	1130	6	AR084610	AR084610 Sequence 2
11	20	100.0	1138	1	EC019114	Y19114 Escherichia
12	20	100.0	1140	6	A23903	A23903 partial seq
13	20	100.0	1140	6	AR059851	AR059851 Sequence
14	20	100.0	1140	6	125094	125094 Sequence 15
15	20	100.0	1489	10	AF128236	AF128236 Mus muscu
16	20	100.0	1518	10	MMCEA4B	AF128236 Mus muscu
17	20	100.0	1842	10	AF113598	AF113598 Mus muscu
18	20	100.0	1878	10	MMCEA4A	AF113598 Mus muscu
19	20	100.0	2043	10	MUSPGGLYD	X98111 M.musculus
20	20	100.0	2538	12	ASPMIN1	M83344 Mouse pregn
21	20	100.0	2646	12	ASPMIN3	Z50148 Artificial
22	20	100.0	3273	12	ARP327	Z50149 Artificial
23	20	100.0	3274	12	SYNPAR327V	V00083 Artificial
24	20	100.0	3302	6	A20357	L08856 pBR327 clon
25	20	100.0	3302	6	A20358	A20357 plasmid pTG
26	20	100.0	3367	6	AX138937	A20358 plasmid pTG
27	20	100.0	3369	6	AX138929	AX138937 Sequence
28	20	100.0	3423	6	A99078	AX138929 Sequence
29	20	100.0	3474	6	A28084	A99078 Sequence 86
30	20	100.0	3474	6	A28085	A28084 pMTNF-MPH p
31	20	100.0	3474	6	A75741	A28085 pMTNF-MPH p
32	20	100.0	3474	6	AR085100	A75741 Sequence 10
33	20	100.0	3658	12	SYNPAR153V	AR085100 Sequence
34	20	100.0	3668	12	SYNPAR327P	L08857 pAT153 clon
35	20	100.0	3773	12	SYNPMW551V	L08857 pBR327par c
36	20	100.0	3779	12	SYNPMW571V	L09154 pMT551 expr
37	20	100.0	3809	12	SYNPMW511V	L09155 pMT571 expr
38	20	100.0	3903	12	PURDI58	L09153 pMT511 expr
39	20	100.0	3903	12	SYNJRDI58V	X01453 Plasmid vec
40	20	100.0	3913	12	EVU51557	L08919 pURDI58 clo
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42	20	100.0	3954	6	AX138934	L08955 pTR53 clon1
43	20	100.0	3976	6	AX138930	AX138934 Sequence
44	20	100.0	4006	12	SYNPKTH606	AX138930 Sequence
45	20	100.0	4009	6	A39734	L08928 pKTH606 clo

ALIGNMENTS

RESULT 1
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LOCUS AX137658 20 bp DNA
DEFINITION Sequence 2 from Patent EP1076096.
ACCESSION AX137658
VERSION AX137658.1 GI:14273843
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Koizumi,S., Nagano,H., Endo,T., Tabata,K. and Ozaki,A.
TITLE Process for producing gdp-fucose
JOURNAL Patent: EP 1076096-A 2 14-FEB-2001;
KYOMA HAKKO KOGYO CO., LTD. (JP)
LOCATION/Qualifiers

FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA"

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Page 2

BASE COUNT 4 a 3 c 9 g 4 t
ORIGIN

Query Match

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gagctgactggttgaagc 20
Db 1 gagctgactggttgaagc 20
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LOCUS AS8755 41 bp DNA
DEFINITION Sequence 1 from Patent WO9700330.
ACCESSION AS8755
VERSION AS8755.1 GI:3714292
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF NUCLEIC ACIDS
HIMMLER GOTTFRIED (AT) 03-JAN-1997;
Other publication AU 5887296 970115
Other publication AT 402203 970325
Other publication AT 100795 960715.
Location/Qualifiers
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RESULT 3

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DEFINITION Sequence 3 from Patent WO9700330.
ACCESSION AS8757
VERSION AS8757.1 GI:3714294
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF NUCLEIC ACIDS
HIMMLER GOTTFRIED (AT) 03-JAN-1997;
Other publication AU 5887296 970115
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Location/Qualifiers
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DEFINITION Sequence 4 from Patent WO9700330.
ACCESSION AS8758
VERSION AS8758.1 GI:3714295
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF NUCLEIC ACIDS
HIMMLER GOTTFRIED (AT) 03-JAN-1997;
Other publication AU 5887296 970115
Other publication AT 402203 970325
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1 gagcctgactggttgaagc 20

RESULT 5

LOCUS NGSP11B 162 bp DNA
DEFINITION N.gonorrhoeae NGSP-18 silent pilin gene. BCT
ACCESSION X60747
VERSION X60747.1 GI:44986
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Submitted (26-JUN-1991) R. Haas, Max-Planck-Institut fuer Biologie,
Abteilung Interaktionsbiologie, Spemannstrasse 34, D-7400 Tuebingen,
FRG
See X60745, X60747-X60751 for related sequences.
Location/Qualifiers
1. .162
/organism="Neisseria gonorrhoeae"
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CDS

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OY 1 gaagctgactgggtgaagc 20
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Db 62 GAGCTGACTGGGTGAAGC 43

RESULT 6
LOCUS E00695 600 bp RNA PAT 29-SEP-1997
DEFINITION A plasmid pGSIT-102 containing a DNA encoding a polypeptide having human gamma-interferon activities.
ACCESSION E00695
VERSION E00695.1 GI:2168972
KEYWORDS JP 1986033200-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 600)
AUTHORS Takahashi Y., Tauchi M., Chiyaaruzu T. and Jiyon R.
TITLE GAMMA-INTERFERON
JOURNAL Patent: JP 1986033200-A 1 17-FEB-1986;
ASAHI CHEM IND CO LTD
OS Homo sapiens
PN JP 1986033200-A/1
PD 17-FEB-1986
PF 22-MAY-1985 JP 1985108299
PI TAKAHASHI YASUYUKI, TAUCHI MASATOSHI, CHIYAARUZU TOTSUO, PI
JIYON ROTSUSHI
PC C07K15/26,A61K45/02,C12N1/20,C12N15/00,C12P21/02,(C12N1/20, PC
C12R1:19),
PC (C12N15/00,C12R1:19),(C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell-type-Monocyte;
CC *source: clone-pgr-101;
FH Key Location/Qualifiers
FT CDS 115..558
FT /product="polypeptide having human
FT gamma-interferon
FT /activities'
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FT gamma-interferon
FT /activities'
FT variation replace(556,'A').
FT Location/Qualifiers
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OY 1 gaagctgactgggtgaagc 20
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Db 600 GAGCTGACTGGGTGAAGC 581

RESULT 7
LOCUS A81874 710 bp DNA circular PAT 21-JAN-2000
DEFINITION Sequence 5 from Patent WO9858080.
ACCESSION A81874
VERSION A81874.1 GI:6731888
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 710)
AUTHORS Soederlind,U.H. and Borrebaeck,C.A.
TITLE A METHOD FOR IN VITRO MOLECULAR EVOLUTION OF PROTEIN FUNCTION
JOURNAL Patent: WO 9858080-A 5 23-DEC-1998;
CRIPPS JOANNA ELIZABETH (GB); SOEDERLIND ULF HANS ESKIL (SE)
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OY 1 gaagctgactgggtgaagc 20
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Db 461 GAGCTGACTGGGTGAAGC 442

RESULT 8
LOCUS ARI20677 710 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6159690.
ACCESSION ARI20677
VERSION ARI20677.1 GI:14104253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 710)
AUTHORS Borrebaeck C,Arnekriester, Soderlind,U,HansEskil and
Ottosson,R,IngridCamilla.
TITLE Method for in vitro molecular evolution of protein function using
JOURNAL exonuclease and amplification
PATENT: US 6159690-A 5 12-DEC-2000;
FEATURES
source 1..710
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|||||
Db 461 GAGCTGACTGGGTGAAGC 442

RESULT 9
I00073/c

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Page 4

Page 4

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REFERENCE      Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
AUTHORS        Escherichia
JOURNAL         1 (bases 1 to 1138)
REFERENCE      Frech,G. and Schwartz,S.
AUTHORS        Unpublished
JOURNAL         2 (bases 1 to 1138)
TITLE          Schwarz,S.P.
FEATURES       Direct submission
                Submitted (18-JUN-1999) S.P. Schwarz, Inst. fuer Tierzucht und
                Tierverhalten, FAL, Dosembergstr. 25-27, 29223 Celle, GERMANY
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                /plasmid="PSC101"
                /db_xref="taxon:562"
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                /note="efflux protein of hybridization class C"
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                /transl_table=11
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                /db_xref="GI:12053582"
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                MOIVQVNGNLILLCFLQMSHKGERRPPIKANKNPVSSFRNAGTIVAAIMVPEP
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Qy 1 gaactactgaggttgaagc 20
Db 596 GAAGCTGACGCGGTGAAGCG 577
RESULT 12
A23903/c
LOCUS A23903 1140 bp DNA
DEFINITION partial sequence of PIC1102.
ACCESSION A23903
VERSION A23903.1 GI:641803
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
REFERENCE 1 (bases 1 to 1140)
AUTHORS Barth,P.T.
JOURNAL Vector
Patent: EP 0502637-A 60 09-SEP-1992;
IMPERIAL CHEMICAL INDUSTRIES PLC
LOCALITY/Qualifiers
1..1140
/organism="synthetic construct"
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143..946
/codon_start=1
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FEATURES
SOURCE
CDS

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BASE COUNT 319 a 256 c 248 g 317 t
ORIGIN
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OESNCGAFASPIQLOBRNGSKFSYDVSTLIPIALMYRCAPPPSSQF"

Query Match 100.0%; Score 20; DB 6; Length 1140;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggtgaagc 20
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Db 1076 GAGCTGACTGGTTGAAGC 1057

RESULT 13
LOCUS AR059851 1140 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 60 from patent US 5840521.
ACCESSION AR059851
VERSION AR059851.1 GI:5986301
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
Unclassified.
REFERENCE 1 (bases 1 to 1140)
AUTHORS Barth,P.Thomas.
TITLE Expression vector containing an inducible selection gene system
JOURNAL Patent: US 5840521-A 60 24-NOV-1998;
FEATURES
Location/Qualifiers
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source /organism="unknown"

BASE COUNT 319 a 257 c 248 g 316 t
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Query Match 100.0%; Score 20; DB 6; Length 1140;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggtgaagc 20
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Db 1076 GAGCTGACTGGTTGAAGC 1057

RESULT 14
LOCUS I25094 1140 bp DNA PAT 07-OCT-1996
DEFINITION Sequence 15 from patent US 5547867.
ACCESSION I25094
VERSION I25094.1 GI:1604964
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1140)
AUTHORS Kara,B.V., Hockney,R.C. and Fitton,J.F.
TITLE Fermentation processes for preparing soluble ricin A
JOURNAL Patent: US 5547867-A 15 20-AUG-1996;
FEATURES
Location/Qualifiers
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source /organism="unknown"

Query Match 100.0%; Score 20; DB 6; Length 1140;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggtgaagc 20
|||||
Db 1076 GAGCTGACTGGTTGAAGC 1057

RESULT 15
AF128236/c
LOCUS AF128236 1489 bp mRNA ROD 31-OCT-1999
DEFINITION Mus musculus pregnancy specific glycoprotein 18 mRNA, complete cds.
ACCESSION AF128236
VERSION AF128236.1 GI:6164607
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1489)
AUTHORS Drexler,G.S., Wessells,J. and Zimmermann,W.
TITLE PSG 18 induces IL-10 in murine macrophages
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1489)
AUTHORS Drexler,G.S., Wessells,J. and Zimmermann,W.
TITLE Direct Submission
JOURNAL Submitted (12-FEB-1999) Pathology, Uniformed Services University of
the Health Sciences, 4301 Jones Bridge Rd., Bethesda, MD 20814, USA
Location/Qualifiers
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/strain="Swiss Webster"
/db_xref="taxon:10090"
/tissue_type="placenta"
59..1489
/note="PSG18"
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/protein_id="AF04463.1"
/db_xref="GI:6164608"

CDS

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LVPASVAAGSILLVHNIPKYLQSLFPWKGLAEPKVEIARARAKNSGEPDASG
RETVASNGSLILQNVTKDGTTLRLTRTRVOMERTHTLQDTSLSLCCDTLDSAQ
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AHSRREIGYNGSLLDVTEKDSGLYTLITIDSNVVYTAHVQVNIHQLVQPMARV
TDSIVRVOSSVYFTCPSDNTGISIRMLFNNQRLQTLERMTLSPSKCOLRIHVYRKDA
GEQCEAFNPVYSKTSLSPLSLATNF"

BASE COUNT 423 a 368 c 335 g 363 t
ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 1489;
Best Local Similarity 100.0%; Pred. No. 6; 9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagctgactggtgaagc 20
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Db 1446 GAGCTGACTGGTTGAAGC 1427

Search completed: December 13, 2001, 15:34:40
Job time: 7674 sec

Fri Dec 14 09:21:15 2001

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